

## SEQUENCE LISTING

<110> Regents of the University of California, The  
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Valerie, Kickhoefer A.  
Sujna, Raval-Fernandes  
Phoebe, Stewart L.

<120> Vault and Vault-like Carrier Molecules

<130> 14399-1PCT

<140> to be assigned

<141> 2004-03-10

<150> 60/453,800

<151> 2003-03-10

<160> 143

<170> PatentIn version 3.2

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Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
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Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
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Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp

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Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val 195 200 205		
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Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr 245 250 255		
Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro 260 265 270		
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Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly 290 295 300		
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&lt;213&gt; Homo sapiens

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Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg  
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Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val  
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Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met  
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Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys  
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Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu  
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Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn  
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Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His  
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Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg  
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Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn  
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Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile  
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Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val  
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Ser Leu Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly  
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Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp  
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Lys His Ile Thr Ser Asn Thr Thr Ala Ala Glu Phe Ile Met Ser Ala  
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Asp Gly His Leu Gln Asp Glu Ser Leu Thr Leu Gln Leu Val Lys Arg  
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Ser Arg Pro His Thr Arg Leu Phe Ala Cys Gly Ile Gly Ser Thr Ala  
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Asn Arg His Val Leu Arg Ile Leu Ser Gln Cys Gly Ala Gly Val  
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Lys Leu His Gln His Val Ser Thr His Ser Asp Ile Leu Ser Leu Lys  
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Asn Gln Cys Leu Ala Thr Leu Pro Asp Leu Lys Thr Met Glu Lys Pro  
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His Gly Tyr Val Ser Ala His Pro Asp Ile Leu Ser Leu Glu Asn Gln  
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Cys Leu Ala Thr Leu Ser Asp Leu Lys Thr Met Glu Lys Pro His Gly  
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His Val Ser Ala His Pro Asp Ile Leu Ser Leu Glu Asn Arg Cys Leu  
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Ala Thr Leu Pro Ser Leu Lys Ser Thr Val Ser Ala Ser Pro Leu Phe  
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Gln Ser Leu Gln Ile Ser His Met Thr Gln Ala Asp Leu Tyr Arg Val  
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Asn Asn Ser Asn Cys Leu Leu Ser Glu Pro Pro Ser Trp Arg Ala Gln  
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His Phe Ser Lys Gly Leu Asp Leu Ser Thr Cys Pro Ile Ala Leu Lys  
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Ser Ile Ser Ala Thr Glu Thr Ala Gln Glu Ala Thr Leu Gly Arg Trp  
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Phe Asp Ser Glu Glu Lys Lys Gly Ala Glu Thr Gln Met Pro Ser Tyr  
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Ser Leu Ser Leu Gly Glu Glu Glu Glu Val Glu Asp Leu Ala Val Lys  
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Leu Thr Ser Gly Asp Ser Glu Ser His Pro Glu Pro Thr Asp His Val  
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Leu Gln Glu Lys Lys Met Ala Leu Leu Ser Leu Leu Cys Ser Thr Leu  
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Val Ser Glu Val Asn Met Asn Asn Thr Ser Asp Pro Thr Leu Ala Ala  
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Ile Phe Glu Ile Cys Arg Glu Leu Ala Leu Leu Glu Pro Glu Phe Ile  
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Leu Lys Ala Ser Leu Tyr Ala Arg Gln Gln Leu Asn Val Arg Asn Val  
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Ala Asn Asn Ile Leu Ala Ile Ala Ala Phe Leu Pro Ala Cys Arg Pro  
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His Leu Arg Arg Tyr Phe Cys Ala Ile Val Gln Leu Pro Ser Asp Trp  
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Ile Gln Val Ala Glu Leu Tyr Gln Ser Leu Ala Glu Gly Asp Lys Asn  
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Lys Leu Val Pro Leu Pro Ala Cys Leu Arg Thr Ala Met Thr Asp Lys  
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Trp Asp Ser Ser Arg Ala Gly Lys Arg Met Lys Leu Ser Arg Pro Glu

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    625                                      630                                      635                                      640  
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    645                                      650                                      655  
 Gln Ala Leu Glu Thr Ala Val Asn Leu Ser Val Lys His Ser Leu Pro  
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    675                                      680                                      685  
 Asp Arg Leu Cys Pro Lys Ser Asn Pro Gln Gly Pro Pro Leu Asn Tyr  
    690                                      695                                      700  
 Ala Leu Leu Leu Ile Gly Met Met Ile Thr Arg Ala Glu Gln Val Asp  
    705                                      710                                      715                                      720



Val Val Leu Cys Gly Gly Asp Thr Leu Lys Thr Ala Val Leu Lys Ala  
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Glu Glu Gly Ile Leu Lys Thr Ala Ile Lys Leu Gln Ala Gln Val Gln  
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Glu Phe Asp Glu Asn Asp Gly Trp Ser Leu Asn Thr Phe Gly Lys Tyr  
 755 760 765

Leu Leu Ser Leu Ala Gly Gln Arg Val Pro Val Asp Arg Val Ile Leu  
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Tyr Trp Gln Arg Val Asn Ser Lys Cys Leu Phe Val Gly Ile Leu Leu  
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Arg Arg Val Gln Tyr Leu Ser Thr Asp Leu Asn Pro Asn Asp Val Thr  
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Leu Ser Gly Cys Thr Asp Ala Ile Leu Lys Phe Ile Ala Glu His Gly  
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Ala Ser His Leu Leu Glu His Val Gly Gln Met Asp Lys Ile Phe Lys  
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Ile Pro Pro Pro Pro Gly Lys Thr Gly Val Gln Ser Leu Arg Pro Leu  
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Glu Glu Asp Thr Pro Ser Pro Leu Ala Pro Val Ser Gln Gln Gly Trp  
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Arg Ser Ile Arg Leu Phe Ile Ser Ser Thr Phe Arg Asp Met His Gly  
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Glu Arg Asp Leu Leu Leu Arg Ser Val Leu Pro Ala Leu Gln Ala Arg  
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Ala Ala Pro His Arg Ile Ser Leu His Gly Ile Asp Leu Arg Trp Gly  
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Val Thr Glu Glu Glu Thr Arg Arg Asn Arg Gln Leu Glu Val Cys Leu  
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Lys Thr Ala Phe Leu Ala Ser Leu Val Ser Ala Leu Gln Ala Pro

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Ala Arg Pro Asp Gln Gly Leu Ala Leu Thr Leu Leu Arg Arg Leu				
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Cys Thr Tyr Leu Arg Gly Gln Leu Lys Glu Pro Gly Ala Leu Pro				
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Ser Thr Tyr Arg Ser Leu Val Trp Glu Leu Gln Gln Arg Leu Leu				
1235		1240		1245
Pro Lys Ser Ala Glu Ser Leu His Pro Gly Gln Thr Gln Val Leu				
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Ile Ile Asp Gly Ala Asp Arg Leu Val Asp Gln Asn Gly Gln Leu				
1265		1270		1275
Ile Ser Asp Trp Ile Pro Lys Lys Leu Pro Arg Cys Val His Leu				
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Val Leu Ser Val Ser Ser Asp Ala Gly Leu Gly Glu Thr Leu Glu				
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Gln Ser Gln Gly Ala His Val Leu Ala Leu Gly Pro Leu Glu Ala				
1310		1315		1320
Ser Ala Arg Ala Arg Leu Val Arg Glu Glu Leu Ala Leu Tyr Gly				
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Lys Arg Leu Glu Glu Ser Pro Phe Asn Asn Gln Met Arg Leu Leu				
1340		1345		1350
Leu Val Lys Arg Glu Ser Gly Arg Pro Leu Tyr Leu Arg Leu Val				
1355		1360		1365
Thr Asp His Leu Arg Leu Phe Thr Leu Tyr Glu Gln Val Ser Glu				
1370		1375		1380
Arg Leu Arg Thr Leu Pro Ala Thr Val Pro Leu Leu Leu Gln His				
1385		1390		1395

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Ile Leu Ser Thr Leu Glu Lys Glu His Gly Pro Asp Val Leu Pro
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Gln Ala Leu Thr Ala Leu Glu Val Thr Arg Ser Gly Leu Thr Val
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Asp Gln Leu His Gly Val Leu Ser Val Trp Arg Thr Leu Pro Lys
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Gly Thr Lys Ser Trp Glu Glu Ala Val Ala Ala Gly Asn Ser Gly
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Asp Pro Tyr Pro Met Gly Pro Phe Ala Cys Leu Val Gln Ser Leu
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Arg Ser Leu Leu Gly Glu Gly Pro Leu Glu Arg Pro Gly Ala Arg
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Leu Cys Leu Pro Asp Gly Pro Leu Arg Thr Ala Ala Lys Arg Cys
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Tyr Gly Lys Arg Pro Gly Leu Glu Asp Thr Ala His Ile Leu Ile
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Ala Ala Gln Leu Trp Lys Thr Cys Asp Ala Asp Ala Ser Gly Thr
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Phe Arg Ser Cys Pro Pro Glu Ala Leu Gly Asp Leu Pro Tyr His
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Leu Leu Gln Ser Gly Asn Arg Gly Leu Leu Ser Lys Phe Leu Thr
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Asn Leu His Val Val Ala Ala His Leu Glu Leu Gly Leu Val Ser
1565                      1570                      1575

Arg Leu Leu Glu Ala His Ala Leu Tyr Ala Ser Ser Val Pro Lys
1580                      1585                      1590

Glu Glu Gln Lys Leu Pro Glu Ala Asp Val Ala Val Phe Arg Thr
1595                      1600                      1605

Phe Leu Arg Gln Gln Ala Ser Ile Leu Ser Gln Tyr Pro Arg Leu
1610                      1615                      1620

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Ser Met Val Glu Leu Trp Ala Trp Arg Glu Gly Ala Arg Leu Ala 1865 1870 1875		
Ala Phe Pro Ala His His Gly Phe Val Ala Ala Ala Leu Phe Leu 1880 1885 1890		
His Ala Gly Cys Gln Leu Leu Thr Ala Gly Glu Asp Gly Lys Val 1895 1900 1905		
Gln Val Trp Ser Gly Ser Leu Gly Arg Pro Arg Gly His Leu Gly 1910 1915 1920		
Ser Leu Ser Leu Ser Pro Ala Leu Ser Val Ala Leu Ser Pro Asp 1925 1930 1935		
Gly Asp Arg Val Ala Val Gly Tyr Arg Ala Asp Gly Ile Arg Ile 1940 1945 1950		
Tyr Lys Ile Ser Ser Gly Ser Gln Gly Ala Gln Gly Gln Ala Leu 1955 1960 1965		
Asp Val Ala Val Ser Ala Leu Ala Trp Leu Ser Pro Lys Val Leu 1970 1975 1980		
Val Ser Gly Ala Glu Asp Gly Ser Leu Gln Gly Trp Ala Leu Lys 1985 1990 1995		
Glu Cys Ser Leu Gln Ser Leu Trp Leu Leu Ser Arg Phe Gln Lys 2000 2005 2010		
Pro Val Leu Gly Leu Ala Thr Ser Gln Glu Leu Leu Ala Ser Ala 2015 2020 2025		
Ser Glu Asp Phe Thr Val Gln Leu Trp Pro Arg Gln Leu Leu Thr 2030 2035 2040		
Arg Pro His Lys Ala Glu Asp Phe Pro Cys Gly Thr Glu Leu Arg 2045 2050 2055		

Gly His Glu Gly Pro Val Ser Cys Cys Ser Phe Ser Thr Asp Gly  
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Gly Ser Leu Ala Thr Gly Gly Arg Asp Arg Ser Leu Leu Cys Trp  
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Asp Val Arg Thr Pro Lys Thr Pro Val Leu Ile His Ser Phe Pro  
 2090 2095 2100

Ala Cys His Arg Asp Trp Val Thr Gly Cys Ala Trp Thr Lys Asp  
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Asn Leu Leu Ile Ser Cys Ser Ser Asp Gly Ser Val Gly Leu Trp  
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Asp Pro Glu Ser Gly Gln Arg Leu Gly Gln Phe Leu Gly His Gln  
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Val Ser Arg Asp Gly Thr Leu Lys Val Trp Asp His Gln Gly Val  
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Glu Leu Thr Ser Ile Pro Ala His Ser Gly Pro Ile Ser His Cys  
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His Pro Leu Leu Val Cys Gln Thr His Thr Leu Leu Gly His Ser  
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Gly Pro Val Arg Ala Ala Ala Val Ser Glu Thr Ser Gly Leu Met  
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Leu Thr Ala Ser Glu Asp Gly Ser Val Arg Leu Trp Gln Val Pro  
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Lys Glu Ala Asp Asp Thr Cys Ile Pro Arg Ser Ser Ala Ala Val  
 2270 2275 2280

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Ser Ala	His Thr Phe Phe	Val	Leu Ser Ala Asp	Glu	Lys Ile Ser
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Glu Trp	Gln Val Lys Leu	Arg	Lys Gly Ser Ala	Pro	Gly Asn Leu
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Thr Ser	Leu Asp Trp Ala	Pro	Asp Gly His Phe	Leu	Ile Leu Ala
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Lys Ala	Asp Leu Lys Leu	Leu	Cys Met Lys Pro	Gly	Asp Ala Pro
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Thr His	Lys Glu Tyr Gly	Ile	Phe Val Leu Gln	Pro	Lys Asp Pro
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Gly Val	Leu Ser Phe Leu	Arg	Gln Lys Glu Ser	Gly	Glu Phe Glu
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Glu Arg	Leu Asn Phe Asp	Ile	Asn Leu Glu Asn	Pro	Ser Arg Thr
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Leu Ile	Ser Ile Thr Gln	Ala	Lys Pro Glu Ser	Glu	Ser Ser Phe
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Leu Cys	Ala Ser Ser Asp	Gly	Ile Leu Trp Asn	Leu	Ala Lys Cys
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Ser Pro	Glu Gly Glu Trp	Thr	Thr Gly Asn Met	Trp	Gln Lys Lys



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Ser Glu Pro Thr Pro His Leu Lys Thr Arg Gln Arg Arg Lys Ile		
2540	2545	2550
His Ser Gly Ser Val Thr Ala Leu His Val Leu Pro Glu Leu Leu		
2555	2560	2565
Val Thr Ala Ser Lys Asp Arg Asp Val Lys Leu Trp Glu Arg Pro		
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Ser Met Gln Leu Leu Gly Leu Phe Arg Cys Glu Gly Ser Val Ser		
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Cys Leu Glu Pro Trp Leu Gly Ala Asn Ser Thr Leu Gln Leu Ala		
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Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
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Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
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Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
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Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
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Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
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Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
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Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
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Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
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Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
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Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
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Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
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Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
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Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
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Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
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Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
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Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
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Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
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Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
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Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 565	570	575
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His 580	585	590
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Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp 610	615	620
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625	630	635 640
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645	650	655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660	665	670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675	680	685
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Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 705	710	715 720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
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Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
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Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met  
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Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
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Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
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Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
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Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
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Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
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Lys Ile His Gly Gln Arg Ser Val Asn Pro Asp Ile Leu Ser Leu Glu
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Asn Arg Cys Leu Thr Leu Leu Pro Asp Leu Gln Pro Met Glu Lys Ile
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His Gly Gln Arg Ser Val His Pro Asp Ile Leu Ser Ser Glu Asn Arg
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Cys Leu Thr Leu Leu Pro Asp Leu Gln Ser Leu Glu Lys Leu Cys Gly
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Val Pro Met Pro Leu Tyr Ser Leu Ser Leu Gly Gly Glu Glu Glu Glu  
 210 215 220

Val Val Gly Ala Pro Val Leu Lys Leu Thr Ser Gly Asp Ser Asp Ser  
 225 230 235 240

His Pro Glu Thr Thr Asp Gln Ile Leu Gln Glu Lys Lys Met Ala Leu  
 245 250 255

Leu Thr Leu Leu Cys Ser Ala Met Ala Ser Ser Val Asn Val Lys Asp  
 260 265 270

Ala Ser Asp Pro Thr Arg Ala Ser Ile His Glu Val Cys Ser Ala Leu  
 275 280 285

Ala Pro Leu Glu Pro Glu Phe Ile Leu Lys Ala Ser Leu Tyr Ala Arg  
 290 295 300

Gln Gln Leu Asn Leu Arg Asp Ile Ala Asn Ile Val Leu Ala Val Ala  
 305 310 315 320

Ala Leu Leu Pro Ala Cys Arg Pro His Val Arg Arg Tyr Tyr Ser Ala  
 325 330 335

Ile Val His Leu Pro Ser Asp Trp Ile Gln Val Ala Glu Phe Tyr Gln  
 340 345 350

Ser Leu Ala Glu Gly Asp Glu Lys Lys Leu Val Pro Leu Pro Ala Cys  
 355 360 365

Leu Arg Ala Ala Met Thr Asp Lys Phe Ala Gln Phe Asp Glu Tyr Gln  
 370 375 380

Leu Ala Lys Tyr Asn Pro Arg Lys His Arg Ser Lys Thr Arg Ser Arg  
 385 390 395 400

Gln Pro Pro Arg Pro Gln Arg Thr Lys Pro Pro Phe Ser Glu Ser Gly  
 405 410 415

Lys Cys Phe Pro Lys Ser Val Trp Pro Leu Lys Asn Glu Gln Ile Ser  
 420 425 430

Phe Glu Ala Ala Tyr Asn Ala Val Ser Glu Lys Lys Arg Leu Pro Arg  
 435 440 445

Phe Thr Leu Lys Lys Leu Val Glu Gln Leu His Ile His Glu Pro Ala  
 450 455 460

Gln His Val Gln Ala Leu Leu Gly Tyr Arg Tyr Pro Ser Thr Leu Glu  
 465 470 475 480

Leu Phe Ser Arg Ser His Leu Pro Gly Pro Trp Asp Ser Ser Arg Ala  
 485 490 495

Gly Gln Arg Met Lys Leu Gln Arg Pro Glu Thr Trp Glu Arg Glu Leu  
 500 505 510

Ser Leu Arg Gly Asn Arg Ala Ser Val Trp Glu Glu Leu Ile Asp Asn  
 515 520 525

Gly Lys Leu Pro Phe Met Ala Met Leu Arg Asn Leu Cys Asn Leu Leu  
 530 535 540

Arg Thr Gly Ile Ser Ala His His His Glu Leu Val Leu Gln Arg Leu  
 545 550 555 560

Gln His Glu Lys Ser Val Ile His Ser Arg Gln Phe Pro Phe Arg Phe  
 565 570 575

Leu Asn Ala His Asp Ser Leu Asp Arg Leu Glu Ala Gln Leu Arg Ser  
 580 585 590

Lys Ala Ser Pro Phe Pro Ser Asn Thr Thr Leu Met Lys Arg Ile Met  
 595 600 605

Ile Arg Asn Ser Lys Lys Ile Lys Arg Pro Ala Asn Pro Arg Tyr Leu

610	615	620
Cys Thr Leu Thr Gln Arg Gln Leu Arg Ala Ala Met Ala Ile Pro Val		
625	630	635 640
Met Tyr Glu His Leu Lys Arg Glu Lys Leu Arg Leu His Lys Ala Arg		
	645	650 655
Gln Trp Thr Cys Asp Leu Glu Leu Leu Glu Arg Tyr Arg Gln Ala Leu		
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Glu Thr Ala Val Asn Ile Ser Val Lys His Asn Leu Pro Pro Leu Pro		
	675	680 685
Gly Arg Thr Leu Leu Val Tyr Leu Thr Asp Ala Asn Ala Asn Arg Leu		
	690	695 700
Cys Pro Lys Ser His Leu Gln Gly Pro Pro Leu Asn Tyr Val Leu Leu		
	705	710 715 720
Leu Ile Gly Met Met Met Ala Arg Ala Glu Gln Thr Thr Val Trp Leu		
	725	730 735
Cys Gly Thr Gly Thr Val Lys Thr Pro Val Leu Thr Ala Asp Glu Gly		
	740	745 750
Ile Leu Lys Thr Ala Ile Lys Leu Gln Ala Gln Val Gln Glu Leu Glu		
	755	760 765
Glu Asn Asp Glu Trp Pro Leu Glu Thr Phe Glu Lys Tyr Leu Leu Ser		
	770	775 780
Leu Ala Val Arg Arg Thr Pro Ile Asp Arg Val Ile Leu Phe Gly Gln		
	785	790 795 800
Arg Met Asp Thr Glu Leu Leu Asn Val Ala Lys Gln Ile Ile Trp Gln		
	805	810 815
His Val Asn Ser Lys Cys Leu Phe Val Ser Val Leu Leu Arg Lys Met		
	820	825 830
Gln Tyr Met Ser Pro Asn Leu Asn Pro Asn Asp Val Thr Leu Ser Gly		
	835	840 845

Cys Thr Asp Gly Ile Leu Lys Phe Ile Ala Glu His Gly Ala Ser Arg  
850 855 860

Leu Leu Glu His Val Gly Gln Leu Asp Lys Ile Phe Lys Ile Pro Pro  
865 870 875 880

Pro Pro Gly Lys Thr Lys Val Ser Pro Leu Arg Pro Leu Glu Glu Asn  
885 890 895

Asn Pro Gly Pro Phe Val Pro Ile Ser Gln His Gly Trp Arg Asn Ile  
900 905 910

Arg Leu Phe Ile Ser Ser Thr Phe Arg Asp Met His Gly Glu Arg Asp  
915 920 925

Leu Leu Met Arg Ser Val Leu Pro Ala Leu Gln Ala Arg Ala Phe Pro  
930 935 940

His Arg Ile Ser Leu His Ala Ile Asp Leu Arg Trp Gly Ile Thr Glu  
945 950 955 960

Glu Glu Thr Arg Arg Asn Arg Gln Leu Glu Val Cys Leu Gly Glu Val  
965 970 975

Glu Asn Ser Gln Leu Phe Val Gly Ile Leu Gly Ser Arg Tyr Gly Tyr  
980 985 990

Thr Pro Pro Ser Tyr Asp Leu Pro Asp His Pro His Phe His Trp Thr  
995 1000 1005

Gln Arg Tyr Pro Ser Gly Arg Ser Val Thr Glu Met Glu Val Met  
1010 1015 1020

Gln Phe Leu Asn Arg Gly Gln Arg Ser Glu Pro Ser Asp Gln Ala  
1025 1030 1035

Leu Ile Tyr Phe Arg Asp Pro Gly Phe Leu Ser Ser Val Pro Asp  
1040 1045 1050

Val Trp Lys Pro Asp Phe Ile Ser Glu Ser Glu Glu Ala Ala His  
1055 1060 1065

Arg Val Ser Glu Leu Lys Arg Phe Leu Gln Glu Gln Lys Glu Val  
1070 1075 1080



Thr Cys	Arg Arg Tyr Ser Cys	Glu Trp Gly Gly Val	Ala Ala Gly
1085	1090	1095	
Arg Pro	Tyr Thr Gly Gly Leu	Glu Glu Phe Gly Gln	Leu Val Leu
1100	1105	1110	
Gln Asp	Val Trp Ser Val Ile	Gln Lys Arg Tyr Leu	Gln Pro Gly
1115	1120	1125	
Ala Gln	Leu Glu Gln Pro Gly	Ser Ile Ser Glu Glu	Asp Leu Ile
1130	1135	1140	
Gln Ala	Ser Phe Gln Gln Leu	Lys Ser Pro Pro Ser	Pro Ala Arg
1145	1150	1155	
Pro Arg	Leu Leu Gln Asp Thr	Val Gln Gln Leu Met	Leu Pro His
1160	1165	1170	
Gly Arg	Leu Ser Leu Val Ile	Gly Gln Ala Gly Gln	Gly Lys Thr
1175	1180	1185	
Ala Phe	Leu Ala Ser Leu Val	Ser Ala Leu Lys Val	Pro Asp Gln
1190	1195	1200	
Pro Asn	Val Ala Pro Phe Val	Phe Phe His Phe Ser	Ala Ala Arg
1205	1210	1215	
Pro Asp	Gln Cys Leu Ala Phe	Asn Leu Leu Arg Arg	Leu Cys Thr
1220	1225	1230	
His Leu	His Gln Lys Leu Gly	Glu Pro Ser Ala Leu	Pro Ser Thr
1235	1240	1245	
Tyr Arg	Gly Leu Val Trp Glu	Leu Gln Gln Lys Leu	Leu Leu Lys
1250	1255	1260	
Ser Ala	Gln Trp Leu Gln Pro	Gly Gln Thr Leu Val	Leu Ile Ile
1265	1270	1275	
Asp Gly	Ala Asp Lys Leu Val	Asp His Asn Gly Gln	Leu Ile Ser
1280	1285	1290	
Asp Trp	Ile Pro Lys Ser Leu	Pro Arg Arg Val His	Leu Val Leu

1295	1300	1305
Ser Val 1310	Ser Ser Asp Ser Gly 1315	Leu Gly Glu Thr Leu Gln Gln Ser 1320
Gln Ser 1325	Ala Tyr Val Val Ala 1330	Leu Gly Ser Leu Val Pro Ser Ser 1335
Arg Ala 1340	Gln Leu Val Arg Glu 1345	Glu Leu Ala Leu Tyr Gly Lys Arg 1350
Leu Glu 1355	Glu Ser Pro Phe Asn 1360	Asn Gln Met Arg Leu Leu Leu Ala 1365
Lys Gln 1370	Gly Ser Ser Leu Pro 1375	Leu Tyr Leu His Leu Val Thr Asp 1380
Tyr Leu 1385	Arg Leu Phe Thr Leu 1390	Tyr Glu Gln Val Ser Glu Arg Leu 1395
Arg Thr 1400	Leu Pro Ala Thr Leu 1405	Pro Leu Leu Leu Gln His Ile Leu 1410
Ser Thr 1415	Leu Glu Gln Glu His 1420	Gly His Asn Val Leu Pro Gln Ala 1425
Leu Thr 1430	Ala Leu Glu Val Thr 1435	His Ser Gly Leu Thr Val Asp Gln 1440
Leu His 1445	Ala Val Leu Ser Thr 1450	Trp Leu Thr Leu Pro Lys Glu Thr 1455
Lys Ser 1460	Trp Glu Glu Ala Val 1465	Ala Ala Ser His Ser Gly Asn Leu 1470
Tyr Pro 1475	Leu Ala Pro Phe Ala 1480	Tyr Leu Val Gln Ser Leu Arg Ser 1485
Leu Leu 1490	Gly Glu Gly Pro Val 1495	Glu Arg Pro Gly Ala Arg Leu Cys 1500
Leu Ser 1505	Asp Gly Pro Leu Arg 1510	Thr Ala Val Lys Arg Arg Tyr Gly 1515

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Phe Leu Thr Thr Phe Asp Gly Leu Leu Glu Leu Trp Asp Leu Gln  
 1745 1750 1755  
 His Gly Cys Trp Val Phe Gln Thr Lys Ala His Gln Tyr Gln Ile  
 1760 1765 1770  
 Thr Gly Cys Cys Leu Ser Pro Asp Arg Arg Leu Leu Ala Thr Val  
 1775 1780 1785  
 Cys Leu Gly Gly Tyr Val Lys Leu Trp Asp Thr Val Gln Gly Gln  
 1790 1795 1800  
 Leu Ala Phe Gln Tyr Thr His Pro Lys Ser Leu Asn Cys Ile Thr  
 1805 1810 1815  
 Phe His Pro Glu Gly Gln Val Val Ala Thr Gly Asn Trp Ser Gly  
 1820 1825 1830  
 Ile Val Thr Phe Phe Gln Ala Asp Gly Leu Lys Val Thr Lys Glu  
 1835 1840 1845  
 Leu Gly Gly Pro Gly Pro Ser Val Arg Thr Leu Ala Phe Ser Ala  
 1850 1855 1860  
 Pro Gly Lys Val Val Ala Leu Gly Arg Ile Asp Gly Thr Val Glu  
 1865 1870 1875  
 Leu Trp Ala Trp Gln Glu Gly Thr Arg Leu Ala Ala Phe Pro Ala  
 1880 1885 1890  
 Gln Cys Gly Gly Val Ser Thr Val Leu Phe Leu His Ala Gly Gly  
 1895 1900 1905  
 Arg Phe Leu Thr Ala Gly Glu Asp Gly Lys Ala Gln Leu Trp Ser  
 1910 1915 1920  
 Gly Phe Leu Gly Arg Pro Arg Gly Cys Leu Gly Ser Leu Tyr Leu  
 1925 1930 1935  
 Ser Pro Ala Leu Ser Val Ala Leu Asn Pro Asp Gly Asp Gln Val  
 1940 1945 1950  
 Ala Val Gly Tyr Arg Gly Asp Gly Ile Lys Ile Tyr Arg Ile Ser

1955	1960	1965
Ser Gly 1970	Pro Gln Glu Ala Gln 1975	Cys Gln Glu Leu Asn Val Ala Val 1980
Ser Ala 1985	Leu Val Trp Leu Ser 1990	Pro Ser Val Leu Val Ser Gly Ala 1995
Glu Asp 2000	Gly Ser Leu His Gly 2005	Trp Met Leu Arg Arg Asn Ser Leu 2010
Gln Ser 2015	Leu Trp Leu Ser Ser 2020	Val Cys Gln Lys Pro Val Leu Gly 2025
Leu Ala 2030	Ala Ser Gln Glu Phe 2035	Leu Ala Ser Ala Ser Glu Asp Phe 2040
Thr Val 2045	Arg Leu Trp Pro Arg 2050	Gln Leu Leu Thr Gln Pro His Ala 2055
Val Glu 2060	Glu Leu Pro Cys Ala 2065	Ala Glu Leu Arg Gly His Glu Gly 2070
Pro Val 2075	Cys Cys Cys Ser Phe 2080	Ser Pro Asp Gly Arg Ile Leu Ala 2085
Thr Ala 2090	Gly Arg Asp Arg Asn 2095	Leu Leu Cys Trp Asp Val Lys Val 2100
Ala Gln 2105	Ala Pro Leu Leu Ile 2110	His Thr Phe Ser Ser Cys His Arg 2115
Asp Trp 2120	Ile Thr Gly Cys Thr 2125	Trp Thr Lys Asp Asn Ile Leu Ile 2130
Ser Cys 2135	Ser Ser Asp Gly Ser 2140	Val Gly Leu Trp Asn Pro Glu Ala 2145
Gly Gln 2150	Gln Leu Gly Gln Phe 2155	Pro Gly His Gln Ser Ala Val Ser 2160
Ala Val 2165	Val Ala Val Glu Glu 2170	His Ile Val Ser Val Ser Arg Asp 2175

Gly Thr	Leu Lys Val Trp	Asp	Arg Gln Gly Val	Glu	Leu Thr Ser
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Ile Pro	Ala His Ser Gly	Pro	Ile Ser Gln Cys	Ala	Ala Ala Leu
2195		2200		2205	
Glu Pro	Arg Pro Ala Gly	Gln	Pro Gly Ser Glu	Leu	Met Val Val
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Thr Val	Gly Leu Asp Gly	Ala	Thr Lys Leu Trp	His	Pro Leu Leu
2225		2230		2235	
Val Cys	Gln Ile His Thr	Leu	Gln Gly His Ser	Gly	Pro Val Thr
2240		2245		2250	
Ala Ala	Ala Ala Ser Glu	Ala	Ser Gly Leu Leu	Leu	Thr Ser Asp
2255		2260		2265	
Asn Ser	Ser Val Arg Leu	Trp	Gln Ile Pro Lys	Glu	Ala Asp Asp
2270		2275		2280	
Thr Cys	Lys Pro Arg Ser	Ser	Ala Val Ile Thr	Ala	Val Ala Trp
2285		2290		2295	
Ala Pro	Asp Gly Ser Leu	Val	Val Ser Gly Asn	Glu	Ala Gly Glu
2300		2305		2310	
Leu Thr	Leu Trp Gln Lys	Ala	Gln Ala Val Ala	Thr	Ala Arg Ala
2315		2320		2325	
Pro Gly	Arg Val Ser Asp	Leu	Ile Trp Cys Ser	Ala	Asn Ala Phe
2330		2335		2340	
Phe Val	Leu Ser Ala Asn	Glu	Asn Val Ser Glu	Trp	Gln Val Glu
2345		2350		2355	
Leu Arg	Lys Gly Ser Thr	Cys	Thr Asn Phe Arg	Leu	Tyr Leu Lys
2360		2365		2370	
Arg Val	Leu Gln Glu Asp	Leu	Gly Val Leu Thr	Gly	Met Ala Leu
2375		2380		2385	
Ala Pro	Asp Gly Gln Ser	Leu	Ile Leu Met Lys	Glu	Asp Val Glu
2390		2395		2400	

Leu	Leu	Gln	Met	Lys	Pro	Gly	Ser	Thr	Pro	Ser	Ser	Ile	Cys	Arg
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Arg	Tyr	Ala	Val	His	Ser	Ser	Ile	Leu	Cys	Thr	Ser	Lys	Asp	Tyr
2420						2425					2430			
Gly	Leu	Phe	Tyr	Leu	Gln	Gln	Gly	Asn	Ser	Gly	Ser	Leu	Ser	Ile
2435						2440					2445			
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2450						2455					2460			
Asn	Leu	Asn	Leu	Asn	Asn	Pro	Asn	Gly	Ser	Pro	Val	Ser	Ile	Thr
2465						2470					2475			
Gln	Ala	Glu	Pro	Glu	Ser	Gly	Ser	Ser	Leu	Leu	Cys	Ala	Thr	Ser
2480						2485					2490			
Asp	Gly	Met	Leu	Trp	Asn	Leu	Ser	Glu	Cys	Thr	Pro	Glu	Gly	Glu
2495						2500					2505			
Trp	Val	Val	Asp	Asn	Ile	Trp	Gln	Lys	Lys	Ser	Arg	Asn	Pro	Lys
2510						2515					2520			
Ser	Arg	Thr	Pro	Gly	Thr	Asp	Ser	Ser	Pro	Gly	Leu	Phe	Cys	Met
2525						2530					2535			
Asp	Ser	Trp	Val	Glu	Pro	Thr	His	Leu	Lys	Ala	Arg	Gln	Cys	Lys
2540						2545					2550			
Lys	Ile	His	Leu	Gly	Ser	Val	Thr	Ala	Leu	His	Val	Leu	Pro	Gly
2555						2560					2565			
Leu	Leu	Val	Thr	Ala	Ser	Glu	Asp	Arg	Asp	Val	Lys	Leu	Trp	Glu
2570						2575					2580			
Arg	Pro	Ser	Met	Gln	Leu	Leu	Gly	Leu	Phe	Arg	Cys	Glu	Gly	Pro
2585						2590					2595			
Val	Ser	Cys	Leu	Glu	Pro	Trp	Met	Glu	Pro	Ser	Ser	Pro	Leu	Gln
2600						2605					2610			
Leu	Ala	Val	Gly	Asp	Ala	Gln	Gly	Asn	Leu	Tyr	Phe	Leu	Ser	Trp

2615

2620

2625

Glu

&lt;210&gt; 13

&lt;211&gt; 7890

&lt;212&gt; DNA

<213> *Rattus norvegicus*

&lt;400&gt; 13

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tgccctgacca tgctctctga catccaaccc ctggagaaaa tacatggaca gagatctgtc	120
aaccagaca tcctgtcctt ggagaaccgg tgccctgacct tgctccctga tctccagccc	180
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&lt;210&gt; 14

&lt;211&gt; 143

&lt;212&gt; RNA

&lt;213&gt; Rattus norvegicus

&lt;400&gt; 14

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<400> 15

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 <212> PRT  
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<220>  
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<400> 16

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 20 25 30

Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys Thr Tyr Ile  
 35 40 45

Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met Arg Met Val Thr  
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Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val Ser Arg Asp  
 65 70 75 80

Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val Arg Leu Arg  
 85 90 95

His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr  
 100 105 110

Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu  
 115 120 125

Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys  
 130 135 140

Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro  
 145 150 155 160

Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu Ile Ile Gln  
 165 170 175

Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys  
 180 185 190

Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr Gly Glu Glu Trp  
 195 200 205

Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val Phe Glu Glu Val  
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Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr Ala Leu His  
 225 230 235 240

Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val Ser Arg Arg  
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Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala His Val  
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Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile Thr Thr Leu  
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Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly Pro Asp Gly  
 290 295 300

Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu Lys Ser Phe  
 305 310 315 320

Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln Asp Val Tyr  
 325 330 335

Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu Gln Pro Leu  
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Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala Gly Asp His  
 355 360 365

Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys Val Glu

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385	390	395 400
Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val Ile Gly Ser		
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Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys Glu Leu Pro		
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Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro Leu Ala Asp		
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Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu Ala Pro Arg		
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Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala Ala Val		
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Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val Phe Gly Pro		
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Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val Leu Ser Leu		
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Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu Cys Leu		
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Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu Thr Ala		
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Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu		
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Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu Phe Ser Val		
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Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg Val Arg		
	580	585 590
Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn Ser Ala		
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Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser Glu Ala Lys  
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Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln Ala Val Phe  
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Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser Val Glu  
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Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu  
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Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu  
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Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys  
 690 695 700

Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu  
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Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr Ala Lys Ala  
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Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser  
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Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu  
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Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu Leu Val Tyr  
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Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala  
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Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu Ala Ile Gly Pro  
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Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys  
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Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Ser  
 835 840 845



Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu Leu Gly Met Gly  
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Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser Gly Pro Ser Pro  
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Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro Gln Ala Pro Gly  
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Asp Asn His Val Val Pro Val Leu Arg  
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 <211> 2718  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens

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 <212> PRT  
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<220>  
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<400> 18

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Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg Met Val Thr  
 50 55 60

Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val Ser Arg Asp  
 65 70 75 80

Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val Arg Leu Arg  
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His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe Pro Leu Tyr  
 100 105 110

Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln Val Val Leu  
 115 120 125

Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe Glu Asp Lys  
 130 135 140

Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe Glu Gly Pro  
 145 150 155 160

Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu Ile Ile Gln  
 165 170 175

Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg Ala Arg Lys

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Thr	Gly	Glu	Glu	Trp	Leu	Val	Thr	Val	Gln	Asp	Thr	Glu	Ala	His	Val
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Pro	Asp	Val	Tyr	Glu	Glu	Val	Leu	Gly	Val	Val	Pro	Ile	Thr	Thr	Leu
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Val	Leu	Ser	Glu	Gln	Gln	Gly	Leu	Leu	Leu	Lys	Ala	Leu	Gln	Pro	Leu
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Tyr	Val	Gln	Asp	Val	Lys	Thr	Gly	Lys	Val	Arg	Ala	Val	Ile	Gly	Ser
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Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro Leu Ala Asp  
 435 440 445

Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser Ala Pro Arg  
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Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala Ala Val  
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Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val Phe Gly Pro  
 485 490 495

Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val Leu Ser Leu  
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Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu Cys Leu  
 515 520 525

Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu Thr Ala  
 530 535 540

Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His Phe Glu  
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Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys Leu Phe Ser Val  
 565 570 575

Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg Val Arg  
 580 585 590

Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn Ser Ala  
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Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met Ser Glu Asp Thr  
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Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp Gln Ala Val Phe  
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Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser Val Glu  
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Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val Gln Leu  
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Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys His Glu  
 675 680 685

Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg Gln Lys  
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Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu Leu Glu  
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Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly Asn Ala Lys Ala  
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Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu Gly Ser  
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Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu Thr Glu  
 755 760 765

Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met Glu Leu Ile Tyr  
 770 775 780

Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln Leu Ala  
 785 790 795 800

Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu Ala Leu Gly Pro  
 805 810 815

Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln Val Lys  
 820 825 830

Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp Gly Ser  
 835 840 845

Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu Leu Gly Leu Gly  
 850 855 860

Ser Asp Gly Gln Pro Pro Ala Gln Lys  
 865 870

<210> 19

&lt;211&gt; 2622

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Rattus norvegicus

&lt;400&gt; 19

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caggtctatg actacagagc caagagagcc cgtgtggtct ttgggcccga gctagtgaca     1500

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&lt;210&gt; 20

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; completely synthesized

&lt;400&gt; 20.

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Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
1           5           10           15

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Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Trp
20           25           30

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&lt;210&gt; 21



<211> 89  
 <212> DNA  
 <213> Artificial Sequence

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 <223> completely synthesized

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 <211> 17  
 <212> PRT  
 <213> Artificial Sequence

<220>  
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<400> 22  
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 1 5 10 15

Pro

<210> 23  
 <211> 51  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> completely synthesized

<400> 23  
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<210> 24  
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 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens

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 1 5 10 15

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Met Ala

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Thr	Glu	Glu	Phe	Ile	Ile	Arg	Ile	Pro	Pro	Tyr	His	Tyr	Ile	His	Val
	35						40					45			
Leu	Asp	Gln	Asn	Ser	Asn	Val	Ser	Arg	Val	Glu	Val	Gly	Pro	Lys	Thr
	50					55					60				
Tyr	Ile	Arg	Gln	Asp	Asn	Glu	Arg	Val	Leu	Phe	Ala	Pro	Met	Arg	Met
65					70					75					80
Val	Thr	Val	Pro	Pro	Arg	His	Tyr	Cys	Thr	Val	Ala	Asn	Pro	Val	Ser
			85						90					95	
Arg	Asp	Ala	Gln	Gly	Leu	Val	Leu	Phe	Asp	Val	Thr	Gly	Gln	Val	Arg
		100						105					110		
Leu	Arg	His	Ala	Asp	Leu	Glu	Ile	Arg	Leu	Ala	Gln	Asp	Pro	Phe	Pro
	115						120					125			
Leu	Tyr	Pro	Gly	Glu	Val	Leu	Glu	Lys	Asp	Ile	Thr	Pro	Leu	Gln	Val
	130					135					140				
Val	Leu	Pro	Asn	Thr	Ala	Leu	His	Leu	Lys	Ala	Leu	Leu	Asp	Phe	Glu
145					150					155					160
Asp	Lys	Asp	Gly	Asp	Lys	Val	Val	Ala	Gly	Asp	Glu	Trp	Leu	Phe	Glu
			165						170					175	
Gly	Pro	Gly	Thr	Tyr	Ile	Pro	Arg	Lys	Glu	Val	Glu	Val	Val	Glu	Ile
			180					185					190		
Ile	Gln	Ala	Thr	Ile	Ile	Arg	Gln	Asn	Gln	Ala	Leu	Arg	Leu	Arg	Ala
	195						200					205			
Arg	Lys	Glu	Cys	Trp	Asp	Arg	Asp	Gly	Lys	Glu	Arg	Val	Thr	Gly	Glu
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Glu	Trp	Leu	Val	Thr	Thr	Val	Gly	Ala	Tyr	Leu	Pro	Ala	Val	Phe	Glu
225					230					235					240
Glu	Val	Leu	Asp	Leu	Val	Asp	Ala	Val	Ile	Leu	Thr	Glu	Lys	Thr	Ala
			245						250					255	

Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val Ser  
 260 265 270

Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu Ala  
 275 280 285

His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile Thr  
 290 295 300

Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly Pro  
 305 310 315 320

Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu Lys  
 325 330 335

Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln Asp  
 340 345 350

Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu Gln  
 355 360 365

Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala Gly  
 370 375 380

Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala Lys  
 385 390 395 400

Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu Asn Glu  
 405 410 415

Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val Ile  
 420 425 430

Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys Glu  
 435 440 445

Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro Leu  
 450 455 460

Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu Ala  
 465 470 475 480

Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn Ala  
 485 490 495

Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val Phe  
                   500                                  505                                  510

Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val Leu  
                   515                                  520                                  525

Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala Leu  
                   530                                  535                                  540

Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile Glu  
                   545                                  550                                  555                                  560

Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp His  
                                   565                                  570'                                  575

Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu Phe  
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Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser Arg  
                   595                                  600                                  605

Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys Asn  
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Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser Glu  
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Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln Ala  
                                   645                                  650                                  655

Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln Ser  
                                   660                                  665                                  670

Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser Val  
                   675                                  680                                  685

Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala Lys  
                   690                                  695                                  700

His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu Arg  
                   705                                  710                                  715                                  720

Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu Leu

725	730	735
Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr Ala 740 745 750		
Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly Glu 755 760 765		
Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile Glu 770 775 780		
Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu Leu 785 790 795 800		
Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln Gln 805 810 815		
Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu Ala Ile 820 825 830		
Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met Gln 835 840 845		
Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr Asp 850 855 860		
Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu Leu Gly 865 870 875 880		
Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser Gly Pro 885 890 895		
Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro Gln Ala 900 905 910		
Pro Gly Asp Asn His Val Val Pro Val Leu Arg 915 920		

&lt;210&gt; 25

&lt;211&gt; 2772

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Homo sapiens

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 gtactgcgct aa 2772

<210> 26

<211> 910

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 26

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
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Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr  
 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly  
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro  
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn  
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly  
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp  
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val  
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala  
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg  
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val  
 275 280 285



Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro  
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His  
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln  
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln  
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg

515	520	525
Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile		
530	535	540
Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr		
545	550	555
Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala		
565	570	575
Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile		
580	585	590
Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe		
595	600	605
His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu		
610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg		
625	630	635
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp		
645	650	655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
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Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
675	680	685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
690	695	700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
705	710	715
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr		
725	730	735
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
740	745	750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu  
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu  
 770 775 780

Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys  
 785 790 795 800

Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr  
 805 810 815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro  
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu  
 835 840 845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly  
 850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala  
 865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala  
 885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg  
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<210> 27

<211> 2733

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 27

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gaccaggctg	tcttccccca	aaacgggctg	gtggtcagca	gtgtggacgt	gcagtcagt	1980
gagcctgtgg	atcagaggac	ccgggacgcc	ctgcaacgca	gcgtccagct	ggccatcgag	2040

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 <213> Artificial Sequence

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<400> 28

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1          5          10          15

```

```

Arg Gly Ser His Met Ala Ser Met Thr Gly Gly Gln Gln Pro Trp Met
          20          25          30

```

```

Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His
          35          40          45

```

```

Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys
          50          55          60

```

```

Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg
65          70          75          80

```

```

Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val
          85          90          95

```

Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val  
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Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe  
 115 120 125

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln  
 130 135 140

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe  
 145 150 155 160

Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe  
 165 170 175

Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu  
 180 185 190

Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg  
 195 200 205

Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly  
 210 215 220

Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe  
 225 230 235 240

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr  
 245 250 255

Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val  
 260 265 270

Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu  
 275 280 285

Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile  
 290 295 300

Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly  
 305 310 315 320

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu  
 325 330 335

Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln  
 340 345 350

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala Leu  
 355 360 365

Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala  
 370 375 380

Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala  
 385 390 395 400

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn  
 405 410 415

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val  
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Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys  
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Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro  
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Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser  
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Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn  
 485 490 495

Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val  
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Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val  
 515 520 525

Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala  
 530 535 540

Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile  
 545 550 555 560

Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp

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His	Phe	Glu	Leu	Lys	Asn	Arg	Asn	Asp	Pro	Ala	Glu	Ala	Ala	Lys	Leu				
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Phe	Ser	Val	Pro	Asp	Phe	Val	Gly	Asp	Ala	Cys	Lys	Ala	Ile	Ala	Ser				
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Arg	Val	Arg	Gly	Ala	Val	Ala	Ser	Val	Thr	Phe	Asp	Asp	Phe	His	Lys				
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Asn	Ser	Ala	Arg	Ile	Ile	Arg	Met	Ala	Val	Phe	Gly	Phe	Glu	Met	Ser				
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Glu	Asp	Thr	Gly	Pro	Asp	Gly	Thr	Leu	Leu	Pro	Lys	Ala	Arg	Asp	Gln				
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Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala	Leu	Gln	Arg	Ser				
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Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg	Gly	Arg	Leu	Glu				
705					710					715					720				
Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys	Ala	Arg	Lys	Glu				
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Leu	Leu	Glu	Leu	Glu	Ala	Met	Ser	Met	Ala	Val	Glu	Ser	Thr	Gly	Asn				
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Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala	Arg	Ile	Glu	Gly				
	755						760					765							
Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln	Ala	Leu	Ala	Ile				
	770					775					780								
Glu	Thr	Glu	Ala	Glu	Leu	Glu	Arg	Val	Lys	Lys	Val	Arg	Glu	Met	Glu				
785					790					795					800				



Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala Gln  
                                     805                                    810                                    815

Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu Ala  
                                     820                                    825                                    830

Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu Met  
                                     835                                    840                                    845

Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile Thr  
                                     850                                    855                                    860

Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu Leu  
                                     865                                    870                                    875                                    880

Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys  
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<220>  
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 <211> 878  
 <212> PRT  
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<220>  
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<400> 30

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 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly  
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro  
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn  
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly  
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp  
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val

165	170	175
Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg 180	185	190
Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val 195	200	205
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala 210	215	220
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu 225	230	235 240
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg 245	250	255
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp 260	265	270
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val 275	280	285
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro 290	295	300
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys 305	310	315 320
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly 325	330	335
Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys 340	345	350
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His 355	360	365
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro 370	375	380
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp 385	390	395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His  
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln  
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala  
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu  
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg  
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp  
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln  
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala  
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg  
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg  
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr  
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile  
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu  
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu  
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys  
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr  
 805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro  
 820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu  
 835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly  
 850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys

865

870

875

&lt;210&gt; 31

&lt;211&gt; 2637

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthesized and *Rattus norvegicus*

&lt;400&gt; 31

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&lt;210&gt; 32

&lt;211&gt; 96

&lt;212&gt; PRT

<213> *Saccharomyces cerevisiae*

&lt;400&gt; 32

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
20 25 30



Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

<210> 33  
 <211> 288  
 <212> DNA  
 <213> *Saccharomyces cerevisiae*

<400> 33  
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 tctcccaaaa ccaaagggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180  
 ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240  
 ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggatta 288

<210> 34  
 <211> 989  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 34

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu  
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln  
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu  
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro

530	535	540
Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His		
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Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val		
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Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr		
	580	585 590
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg		
	595	600 605
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr		
	610	615 620
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn		
625	630	635 640
Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys		
	645	650 655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala		
	660	665 670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His		
	675	680 685
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr		
	690	695 700
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp		
705	710	715 720
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val		
	725	730 735
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg		
	740	745 750
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala		
	755	760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly  
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Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg  
 980 985

<210> 35  
 <211> 2970

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> *Saccharomyces cerevisiae* and *Homo sapiens*

&lt;400&gt; 35

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gagttcatca tccgcatccc ccataccac tatatccatg tgctggacca gaacagcaac	360
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&lt;210&gt; 36

&lt;211&gt; 957

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> *Saccharomyces cerevisiae* and *Rattus norvegicus*

&lt;400&gt; 36

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu  
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
225 230 235 240



Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
355 360 365

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met  
370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile  
405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln

465	470	475	480
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala	485	490	495
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu	500	505	510
Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp	515	520	525
Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro	530	535	540
Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His	545	550	555
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val	565	570	575
Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr	580	585	590
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg	595	600	605
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr	610	615	620
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn	625	630	635
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys	645	650	655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala	660	665	670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His	675	680	685
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met	690	695	700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp  
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly  
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met  
 850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys  
 945 950 955

<210> 37  
 <211> 2874  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> *Saccharomyces cerevisiae* and *Rattus norvegicus*

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<210> 38  
 <211> 130  
 <212> PRT  
 <213> Levivirus

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Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
 115 120 125

Ile Tyr  
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<210> 39  
 <211> 393  
 <212> DNA  
 <213> Levivirus

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 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360  
 tcagcaatcg cagcaaactc cggcatctac ccc 393

<210> 40  
 <211> 1024  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Homo sapiens

<400> 40

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr  
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
 115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr  
 130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu  
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe  
 165 170 175

Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val  
 180 185 190

Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val  
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala  
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile  
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala  
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp  
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val  
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala  
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp  
 355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430



Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu  
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro  
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys  
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val  
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys  
 545 550 555 560

Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser  
 565 570 575

Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg  
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg  
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu  
 610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His  
 625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp  
 645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu

660	665	670
Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu 675 680 685		
Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys 690 695 700		
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp 705 710 715 720		
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly 725 730 735		
Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg 740 745 750		
Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser 755 760 765		
Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala 770 775 780		
Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln 785 790 795 800		
Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg 805 810 815		
Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys 820 825 830		
Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu 835 840 845		
Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala 850 855 860		
Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln 865 870 875 880		
Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val 885 890 895		

Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val  
                   900                                  905                                  910

Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln  
                   915                                  920                                  925

Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala  
                   930                                  935                                  940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser  
                   945                                  950                                  955                                  960

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala  
                                   965                                  970                                  975

Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg  
                   980                                  985                                  990

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala  
                   995                                  1000                                  1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu  
                   1010                                  1015                                  1020

Arg

<210> 41  
 <211> 3075  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Homo sapiens

<400> 41  
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 caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc 180  
 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gtttctgtga 240  
 gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300  
 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360  
 tcagcaatcg cagcaaactc cggcatctac cccatggcaa ctgaagagtt catcatccgc 420

atccccccat accactatat ccatgtgctg gaccagaaca gcaacgtgtc ccgtgtggag	480
gtcggggccaa agacctacat ccggcaggac aatgagaggg tactgtttgc ccccatgcgc	540
atggtgaccg tccccccacg tcactactgc acagtggcca accctgtgtc tcgggatgcc	600
cagggcttgg tgctgtttga tgtcacaggg caagttcggc ttcgccacgc tgacctcgag	660
atccggctgg cccaggaccc cttccccctg taccagggg aggtgctgga aaaggacatc	720
acaccctgc aggtggttct gccaacact gccctccatc taaaggcgct gcttgatttt	780
gaggataaag atggagacaa ggtggtggca ggagatgagt ggcttttcga gggacctggc	840
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cagaaccagg ctctgcggct cagggcccgc aaggagtgtc gggaccggga cggcaaggag	960
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cgggctcggc ggaacttccg ggacttcagg ggagtgtccc gccgcactgg ggaggagtgg	1140
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gcccgcctg cgctctgcct gctgctgggg cctgacttct tcacagacgt catcaccatc	1980
gaaacggcgg atcatgccag gctgcaactg cagctggcct acaactggca ctttgagggtg	2040
aatgaccgga aggaccccc aagagacggc aagctctttt cagtgccaga ctttgtaggt	2100
gatgcctgca aagccatcgc atccgggtg cggggggccg tggcctctgt cactttcgat	2160

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gacttccata agaactcagc ccgcatcatt cgcactgctg tctttggctt tgagacctcg 2220
gaagcgaagg gccccgatgg catggccctg cccaggcccc gggaccaggc tgtcttcccc 2280
caaaacgggc tggtaggtcag cagtgtggac gtgcagtcag tggagcctgt ggatcagagg 2340
acccgggacg ccctgcaacg cagcgtccag ctggccatcg agatcaccac caactcccag 2400
gaagcggcgg ccaagcatga ggctcagaga ctggagcagg aagcccgcgg ccggcttgag 2460
cggcagaaga tcctggacca gtcagaagcc gagaaagctc gcaaggaact tttggagctg 2520
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cctgtactgc gctaa 3075

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<210> 42  
 <211> 992  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Rattus norvegicus

<400> 42

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Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10          15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20          25          30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
          35          40          45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
          50          55          60

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr  
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu  
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe  
165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val  
180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile  
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala  
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile  
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala  
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp  
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val  
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala  
290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp  
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu  
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro  
 500 505 510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys  
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val

530	535	540
Leu Trp Glu Lys Glu 545	Leu Pro Ser Gly Val 550	Glu Glu Leu Leu Asn Leu 555 560
Gly His Asp Pro 565	Leu Ala Asp Arg Gly 570	Lys Gly Thr Ala Lys Pro 575
Leu Gln Pro Ser Ala 580	Pro Arg Asn Lys Thr 585	Arg Val Val Ser Tyr Arg 590
Val Pro His Asn Ala 595	Ala Val Gln Val Tyr 600	Asp Tyr Arg Ala Lys Arg 605
Ala Arg Val Val Phe 610	Gly Pro Glu Leu Val 615	Thr Leu Asp Pro Glu Glu 620
Gln Phe Thr Val Leu 625	Ser Leu Ser Ala Gly 630	Arg Pro Lys Arg Pro His 635 640
Ala Arg Arg Ala Leu 645	Cys Leu Leu Leu Gly 650	Pro Asp Phe Phe Thr Asp 655
Val Ile Thr Ile Glu 660	Thr Ala Asp His Ala 665	Arg Leu Gln Leu Gln Leu 670
Ala Tyr Asn Trp His 675	Phe Glu Leu Lys Asn 680	Arg Asn Asp Pro Ala Glu 685
Ala Ala Lys Leu Phe 690	Ser Val Pro Asp Phe 695	Val Gly Asp Ala Cys Lys 700
Ala Ile Ala Ser Arg 705	Val Arg Gly Ala Val 710	Ala Ser Val Thr Phe Asp 715 720
Asp Phe His Lys Asn 725	Ser Ala Arg Ile Ile 730	Arg Met Ala Val Phe Gly 735
Phe Glu Met Ser Glu 740	Asp Thr Gly Pro Asp 745	Gly Thr Leu Leu Pro Lys 750
Ala Arg Asp Gln Ala 755	Val Phe Pro Gln Asn 760	Gly Leu Val Val Ser Ser 765



Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala  
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln  
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg  
 805 810 815

Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys  
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu  
 835 840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala  
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln  
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val  
 885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val  
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu  
 915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala  
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser  
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala  
 965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys  
 980 985 990

<210> 43

<211> 2979

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Levivirus and Rattus norvegicus

&lt;400&gt; 43

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caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc	180
atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gcttcctgta	240
gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc	300
gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc	360
tcagcaatcg cagcaaactc cgcatctac cccatggcaa ctgaagaggc catcatccgc	420
atcccccat accactacat ccatgtgctg gaccagaaca gtaatgtgtc ccgtgtggag	480
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atggtgaccg tccccccacg ccactactgc atagtggcca accctgtgtc ccgggacacc	600
cagagttctg tgttatttga catcacagga caagtccgac tccggcacgc tgaccaggag	660
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acccactgc aggtggttct gcccaacaca gcactgcac ttaaggcggt gctggacttt	780
gaggataaga atggagacaa ggtcatggca ggagacgagt ggctatttga gggacctggc	840
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cagaaccaag cactgcggct aaggggcccga aaggagtgtc ttgaccggga gggcaagggg	960
cgctgacag gtgaggagtg gctggtccga tccgtggggg cttacctccc agctgtcttt	1020
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caggggctgc tactgaaggc actgcagccc ctggaggagg gagagagcga ggagaaggtc	1440
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aaagtggagg tgggtggagga gcgtcaggct atccctctgg accaaaatga gggcatctat	1560

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actctcatca ccgatggctc gtctcccatc aacctcttca gcacagcctt cgggttgctg 2940
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&lt;210&gt; 44

&lt;211&gt; 239

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; completely synthesized

&lt;400&gt; 44

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro  
 225 230 235

<210> 45  
 <211> 720  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> completely synthesized

<400> 45  
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 gatgtgaatg ggcacaaatt ttctgtcagc ggagaggggtg aaggatgatgc cacatacggg 120  
 aagctcaccg tgaaattcat ctgcaccact ggaaagctcc ctgtgccatg gccaacactg 180  
 gtcactacct tcacctatgg cgtgcagtgc ttttccagat acccagacca tatgaagcag 240  
 catgactttt tcaagagcgc catgcccagag ggctatgtgc aggagagaac catctttttc 300  
 aaagatgacg ggaactacaa gaccgcgcgt gaagtcaagt tcgaagggtga caccctgggtg 360  
 aatagaatcg agctgaaggg cattgacttt aaggaggatg gaaacattct cggccacaag 420  
 ctggaataca actataactc ccacaatgtg tacatcatgg ccgacaagca aaagaatggc 480  
 atcaagggtca acttcaagat cagacacaac attgaggatg gatccgtgca gctggccgac 540  
 cattatcaac agaactctcc aatcgggcgc ggccctgtgc tcctcccaga caaccattac 600  
 ctgtccaccc agtctgccct gtctaaagat cccaacgaaa agagagacca catgggtcctg 660  
 ctggagtttg tgaccgctgc tgggatcaca catggcatgg acgagctgta caagcccatg 720

<210> 46  
 <211> 1132  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens

<400> 46

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
 1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe

50	55	60															
Thr	Tyr	Gly	Val	Gln	Cys	Phe	Ser	Arg	Tyr	Pro	Asp	His	Met	Lys	Gln		
65					70					75					80		
His	Asp	Phe	Phe	Lys	Ser	Ala	Met	Pro	Glu	Gly	Tyr	Val	Gln	Glu	Arg		
				85					90					95			
Thr	Ile	Phe	Phe	Lys	Asp	Asp	Gly	Asn	Tyr	Lys	Thr	Arg	Ala	Glu	Val		
			100					105						110			
Lys	Phe	Glu	Gly	Asp	Thr	Leu	Val	Asn	Arg	Ile	Glu	Leu	Lys	Gly	Ile		
		115					120					125					
Asp	Phe	Lys	Glu	Asp	Gly	Asn	Ile	Leu	Gly	His	Lys	Leu	Glu	Tyr	Asn		
	130					135					140						
Tyr	Asn	Ser	His	Asn	Val	Tyr	Ile	Met	Ala	Asp	Lys	Gln	Lys	Asn	Gly		
145					150					155					160		
Ile	Lys	Val	Asn	Phe	Lys	Ile	Arg	His	Asn	Ile	Glu	Asp	Gly	Ser	Val		
			165						170					175			
Gln	Leu	Ala	Asp	His	Tyr	Gln	Gln	Asn	Thr	Pro	Ile	Gly	Asp	Gly	Pro		
			180					185					190				
Val	Leu	Leu	Pro	Asp	Asn	His	Tyr	Leu	Ser	Thr	Gln	Ser	Ala	Leu	Ser		
		195					200					205					
Lys	Asp	Pro	Asn	Glu	Lys	Arg	Asp	His	Met	Val	Leu	Leu	Glu	Phe	Val		
	210					215					220						
Thr	Ala	Ala	Gly	Ile	Thr	His	Gly	Met	Asp	Glu	Leu	Tyr	Lys	Pro	Met		
225					230					235					240		
Ala	Thr	Glu	Glu	Phe	Ile	Ile	Arg	Ile	Pro	Pro	Tyr	His	Tyr	Ile	His		
				245					250					255			
Val	Leu	Asp	Gln	Asn	Ser	Asn	Val	Ser	Arg	Val	Glu	Val	Gly	Pro	Lys		
		260						265					270				
Thr	Tyr	Ile	Arg	Gln	Asp	Asn	Glu	Arg	Val	Leu	Phe	Ala	Pro	Met	Arg		
	275					280						285					

Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro Val  
 290 295 300

Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln Val  
 305 310 315 320

Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro Phe  
 325 330 335

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln  
 340 345 350

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe  
 355 360 365

Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu Phe  
 370 375 380

Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val Glu  
 385 390 395 400

Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu Arg  
 405 410 415

Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr Gly  
 420 425 430

Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val Phe  
 435 440 445

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr  
 450 455 460

Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly Val  
 465 470 475 480

Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu  
 485 490 495

Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro Ile  
 500 505 510

Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val Gly  
 515 520 525

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu  
 530 535 540

Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile Gln  
 545 550 555 560

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala Leu  
 565 570 575

Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln Ala  
 580 585 590

Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala  
 595 600 605

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu Asn  
 610 615 620

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val  
 625 630 635 640

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys  
 645 650 655

Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp Pro  
 660 665 670

Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro Leu  
 675 680 685

Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn  
 690 695 700

Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val Val  
 705 710 715 720

Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr Val  
 725 730 735

Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala  
 740 745 750

Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile



755	760	765
Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp 770 775 780		
His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys Leu 785 790 795 800		
Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser 805 810 815		
Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys 820 825 830		
Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr Ser 835 840 845		
Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp Gln 850 855 860		
Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln 865 870 875 880		
Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg Ser 885 890 895		
Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala Ala 900 905 910		
Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu Glu 915 920 925		
Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys Glu 930 935 940		
Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly Thr 945 950 955 960		
Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu Gly 965 970 975		
Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala Ile 980 985 990		

Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu Glu  
 995 1000 1005

Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 1010 1015 1020

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr  
 1025 1030 1035

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly  
 1040 1045 1050

Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser  
 1055 1060 1065

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr  
 1070 1075 1080

Ala Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly  
 1085 1090 1095

Arg Arg Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro  
 1100 1105 1110

Gln Ser Ala Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val  
 1115 1120 1125

Pro Val Leu Arg  
 1130

<210> 47  
 <211> 3399  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens

<400> 47

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 1 5 10 15

Ala Ala Cys Thr Gly Thr Thr Cys Ala Cys Thr Gly Gly Cys Gly Thr  
 20 25 30

Gly Gly Thr Cys Cys Cys Ala Ala Thr Thr Cys Thr Cys Gly Thr Gly  
 35 40 45

Gly Ala Ala Cys Thr Gly Gly Ala Thr Gly Gly Cys Gly Ala Thr Gly  
 50 55 60

Thr Gly Ala Ala Thr Gly Gly Gly Cys Ala Cys Ala Ala Ala Thr Thr  
 65 70 75 80

Thr Thr Cys Thr Gly Thr Cys Ala Gly Cys Gly Gly Ala Gly Ala Gly  
 85 90 95

Gly Gly Thr Gly Ala Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Ala  
 100 105 110

Cys Ala Thr Ala Cys Gly Gly Ala Ala Ala Gly Cys Thr Cys Ala Cys  
 115 120 125

Cys Cys Thr Gly Ala Ala Ala Thr Thr Cys Ala Thr Cys Thr Gly Cys  
 130 135 140

Ala Cys Cys Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys Thr Cys Cys  
 145 150 155 160

Cys Thr Gly Thr Gly Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala Cys  
 165 170 175

Ala Cys Thr Gly Gly Thr Cys Ala Cys Thr Ala Cys Cys Thr Thr Cys  
 180 185 190

Ala Cys Cys Thr Ala Thr Gly Gly Cys Gly Thr Gly Cys Ala Gly Thr  
 195 200 205

Gly Cys Thr Thr Thr Thr Cys Cys Ala Gly Ala Thr Ala Cys Cys Cys  
 210 215 220

Ala Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Ala Gly Cys Ala Gly  
 225 230 235 240

Cys Ala Thr Gly Ala Cys Thr Thr Thr Thr Thr Cys Ala Ala Gly Ala  
 245 250 255

Gly Cys Gly Cys Cys Ala Thr Gly Cys Cys Cys Gly Ala Gly Gly Gly  
 260 265 270

Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Gly Ala Gly Ala  
 275 280 285

Ala Cys Cys Ala Thr Cys Thr Thr Thr Thr Thr Cys Ala Ala Ala Gly  
 290 295 300

Ala Thr Gly Ala Cys Gly Gly Gly Ala Ala Cys Thr Ala Cys Ala Ala  
 305 310 315 320

Gly Ala Cys Cys Cys Gly Cys Gly Cys Thr Gly Ala Ala Gly Thr Cys  
 325 330 335

Ala Ala Gly Thr Thr Cys Gly Ala Ala Gly Gly Thr Gly Ala Cys Ala  
 340 345 350

Cys Cys Cys Thr Gly Gly Thr Gly Ala Ala Thr Ala Gly Ala Ala Thr  
 355 360 365

Cys Gly Ala Gly Cys Thr Gly Ala Ala Gly Gly Gly Cys Ala Thr Thr  
 370 375 380

Gly Ala Cys Thr Thr Thr Ala Ala Gly Gly Ala Gly Gly Ala Thr Gly  
 385 390 395 400

Gly Ala Ala Ala Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Cys Ala  
 405 410 415

Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala Thr Ala Cys Ala Ala Cys  
 420 425 430

Thr Ala Thr Ala Ala Cys Thr Cys Cys Cys Ala Cys Ala Ala Thr Gly  
 435 440 445

Thr Gly Thr Ala Cys Ala Thr Cys Ala Thr Gly Gly Cys Cys Gly Ala  
 450 455 460

Cys Ala Ala Gly Cys Ala Ala Ala Ala Gly Ala Ala Thr Gly Gly Cys  
 465 470 475 480

Ala Thr Cys Ala Ala Gly Gly Thr Cys Ala Ala Cys Thr Thr Cys Ala  
 485 490 495

Ala Gly Ala Thr Cys Ala Gly Ala Cys Ala Cys Ala Ala Cys Ala Thr

500	505	510
Thr Gly Ala Gly Gly Ala	Thr Gly Gly Ala Thr	Cys Cys Gly Thr Gly
515	520	525
Cys Ala Gly Cys Thr Gly	Gly Cys Cys Gly Ala	Cys Cys Ala Thr Thr
530	535	540
Ala Thr Cys Ala Ala Cys	Ala Gly Ala Ala Cys	Ala Cys Thr Cys Cys
545	550	555
Ala Ala Thr Cys Gly Gly	Cys Gly Ala Cys Gly Gly	Cys Cys Cys Thr
565	570	575
Gly Thr Gly Cys Thr Cys	Cys Cys Thr Cys Cys	Ala Gly Ala Cys Ala
580	585	590
Ala Cys Cys Ala Thr Thr	Ala Cys Cys Thr Gly Thr	Cys Cys Ala Cys
595	600	605
Cys Cys Ala Gly Thr Cys	Thr Gly Cys Cys Cys	Thr Gly Thr Cys Thr
610	615	620
Ala Ala Ala Gly Ala Thr	Cys Cys Cys Ala Ala	Cys Gly Ala Ala Ala
625	630	635
Ala Gly Ala Gly Ala Gly	Ala Cys Cys Ala Thr	Gly Gly Thr
645	650	655
Cys Cys Thr Gly Cys Thr	Gly Gly Ala Gly Thr Thr	Thr Gly Thr Gly
660	665	670
Ala Cys Cys Gly Cys Thr	Gly Cys Thr Gly Gly	Gly Ala Thr Cys Ala
675	680	685
Cys Ala Cys Ala Thr Gly	Gly Cys Ala Thr Gly	Gly Ala Cys Gly Ala
690	695	700
Gly Cys Thr Gly Thr Ala	Cys Ala Ala Gly Cys	Cys Cys Ala Thr Gly
705	710	715
Gly Cys Ala Ala Cys Thr	Gly Ala Ala Gly Thr Thr	Cys Ala
725	730	735

Thr Cys Ala Thr Cys Cys Gly Cys Ala Thr Cys Cys Cys Cys Cys Cys  
 740 745 750

Ala Thr Ala Cys Cys Ala Cys Thr Ala Thr Ala Thr Cys Cys Ala Thr  
 755 760 765

Gly Thr Gly Cys Thr Gly Gly Ala Cys Cys Ala Gly Ala Ala Cys Ala  
 770 775 780

Gly Cys Ala Ala Cys Gly Thr Gly Thr Cys Cys Cys Gly Thr Gly Thr  
 785 790 795 800

Gly Gly Ala Gly Gly Thr Cys Gly Gly Gly Cys Cys Ala Ala Ala Gly  
 805 810 815

Ala Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Cys Ala Gly Gly  
 820 825 830

Ala Cys Ala Ala Thr Gly Ala Gly Ala Gly Gly Gly Thr Ala Cys Thr  
 835 840 845

Gly Thr Thr Thr Gly Cys Cys Cys Cys Cys Ala Thr Gly Cys Gly Cys  
 850 855 860

Ala Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr Cys Cys Cys Cys Cys  
 865 870 875 880

Cys Ala Cys Gly Thr Cys Ala Cys Thr Ala Cys Thr Gly Cys Ala Cys  
 885 890 895

Ala Gly Thr Gly Gly Cys Cys Ala Ala Cys Cys Cys Thr Gly Thr Gly  
 900 905 910

Thr Cys Thr Cys Gly Gly Gly Ala Thr Gly Cys Cys Cys Ala Gly Gly  
 915 920 925

Gly Cys Thr Thr Gly Gly Thr Gly Cys Thr Gly Thr Thr Thr Gly Ala  
 930 935 940

Thr Gly Thr Cys Ala Cys Ala Gly Gly Gly Cys Ala Ala Gly Thr Thr  
 945 950 955 960

Cys Gly Gly Cys Thr Thr Cys Gly Cys Cys Ala Cys Gly Cys Thr Gly  
 965 970 975

Ala Cys Cys Thr Cys Gly Ala Gly Ala Thr Cys Cys Gly Gly Cys Thr  
 980 985 990

Gly Gly Cys Cys Cys Ala Gly Gly Ala Cys Cys Cys Cys Thr Thr Cys  
 995 1000 1005

Cys Cys Cys Cys Thr Gly Thr Ala Cys Cys Cys Ala Gly Gly Gly  
 1010 1015 1020

Gly Ala Gly Gly Thr Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly  
 1025 1030 1035

Gly Ala Cys Ala Thr Cys Ala Cys Ala Cys Cys Cys Cys Thr Gly  
 1040 1045 1050

Cys Ala Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Cys Cys Cys  
 1055 1060 1065

Ala Ala Cys Ala Cys Thr Gly Cys Cys Cys Thr Cys Cys Ala Thr  
 1070 1075 1080

Cys Thr Ala Ala Ala Gly Gly Cys Gly Cys Thr Gly Cys Thr Thr  
 1085 1090 1095

Gly Ala Thr Thr Thr Thr Gly Ala Gly Gly Ala Thr Ala Ala Ala  
 1100 1105 1110

Gly Ala Thr Gly Gly Ala Gly Ala Cys Ala Ala Gly Gly Thr Gly  
 1115 1120 1125

Gly Thr Gly Gly Cys Ala Gly Gly Ala Gly Ala Thr Gly Ala Gly  
 1130 1135 1140

Thr Gly Gly Cys Thr Thr Thr Thr Cys Gly Ala Gly Gly Gly Ala  
 1145 1150 1155

Cys Cys Thr Gly Gly Cys Ala Cys Gly Thr Ala Cys Ala Thr Cys  
 1160 1165 1170

Cys Cys Cys Cys Gly Gly Ala Ala Gly Gly Ala Ala Gly Thr Gly  
 1175 1180 1185

Gly Ala Gly Gly Thr Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys

1190	1195	1200
Ala Thr Thr Cys Ala Gly Gly Cys Cys Ala Cys Cys Ala Thr Cys 1205 1210 1215		
Ala Thr Cys Ala Gly Gly Cys Ala Gly Ala Ala Cys Cys Ala Gly 1220 1225 1230		
Gly Cys Thr Cys Thr Gly Cys Gly Gly Cys Thr Cys Ala Gly Gly 1235 1240 1245		
Gly Cys Cys Cys Gly Cys Ala Ala Gly Gly Ala Gly Thr Gly Cys 1250 1255 1260		
Thr Gly Gly Gly Ala Cys Cys Gly Gly Gly Ala Cys Gly Gly Cys 1265 1270 1275		
Ala Ala Gly Gly Ala Gly Ala Gly Gly Gly Thr Gly Ala Cys Ala 1280 1285 1290		
Gly Gly Gly Gly Ala Ala Gly Ala Ala Thr Gly Gly Cys Thr Gly 1295 1300 1305		
Gly Thr Cys Ala Cys Cys Ala Cys Ala Gly Thr Ala Gly Gly Gly 1310 1315 1320		
Gly Cys Gly Thr Ala Cys Cys Thr Cys Cys Cys Ala Gly Cys Gly 1325 1330 1335		
Gly Thr Gly Thr Thr Thr Gly Ala Gly Gly Ala Gly Gly Thr Thr 1340 1345 1350		
Cys Thr Gly Gly Ala Thr Thr Thr Gly Gly Thr Gly Gly Ala Cys 1355 1360 1365		
Gly Cys Cys Gly Thr Cys Ala Thr Cys Cys Thr Thr Ala Cys Gly 1370 1375 1380		
Gly Ala Ala Ala Ala Gly Ala Cys Ala Gly Cys Cys Cys Thr Gly 1385 1390 1395		
Cys Ala Cys Cys Thr Cys Cys Gly Gly Gly Cys Thr Cys Gly Gly 1400 1405 1410		



Cys Gly Gly Ala Ala Cys Thr Thr Cys Cys Gly Gly Gly Ala Cys  
 1415 1420 1425

Thr Thr Cys Ala Gly Gly Gly Gly Ala Gly Thr Gly Thr Cys Cys  
 1430 1435 1440

Cys Gly Cys Cys Gly Cys Ala Cys Thr Gly Gly Gly Gly Ala Gly  
 1445 1450 1455

Gly Ala Gly Thr Gly Gly Cys Thr Gly Gly Thr Ala Ala Cys Ala  
 1460 1465 1470

Gly Thr Gly Cys Ala Gly Gly Ala Cys Ala Cys Ala Gly Ala Gly  
 1475 1480 1485

Gly Cys Cys Cys Ala Cys Gly Thr Gly Cys Cys Ala Gly Ala Thr  
 1490 1495 1500

Gly Thr Cys Cys Ala Cys Gly Ala Gly Gly Ala Gly Gly Thr Gly  
 1505 1510 1515

Cys Thr Gly Gly Gly Gly Gly Thr Thr Gly Thr Gly Cys Cys Cys  
 1520 1525 1530

Ala Thr Cys Ala Cys Cys Ala Cys Cys Cys Thr Gly Gly Gly Cys  
 1535 1540 1545

Cys Cys Cys Cys Ala Cys Ala Ala Cys Thr Ala Cys Thr Gly Cys  
 1550 1555 1560

Gly Thr Gly Ala Thr Thr Cys Thr Cys Gly Ala Cys Cys Cys Thr  
 1565 1570 1575

Gly Thr Cys Gly Gly Ala Cys Cys Gly Gly Ala Thr Gly Gly Cys  
 1580 1585 1590

Ala Ala Gly Ala Ala Thr Cys Ala Gly Cys Thr Gly Gly Gly Gly  
 1595 1600 1605

Cys Ala Gly Ala Ala Gly Cys Gly Cys Gly Thr Gly Gly Thr Cys  
 1610 1615 1620

Ala Ala Gly Gly Gly Ala Gly Ala Gly Ala Ala Gly Thr Cys Thr  
 1625 1630 1635

Thr Thr Thr Thr Thr Cys Cys Thr Cys Cys Ala Gly Cys Cys Ala  
 1640 1645 1650

Gly Gly Ala Gly Ala Gly Cys Ala Gly Cys Thr Gly Gly Ala Ala  
 1655 1660 1665

Cys Ala Ala Gly Gly Cys Ala Thr Cys Cys Ala Gly Gly Ala Thr  
 1670 1675 1680

Gly Thr Gly Thr Ala Thr Gly Thr Gly Cys Thr Gly Thr Cys Gly  
 1685 1690 1695

Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly Cys Thr Gly  
 1700 1705 1710

Cys Thr Gly Cys Thr Gly Ala Gly Gly Gly Cys Cys Cys Thr Gly  
 1715 1720 1725

Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly Gly Ala Gly  
 1730 1735 1740

Gly Gly Gly Gly Ala Gly Gly Ala Thr Gly Ala Gly Gly Ala Gly  
 1745 1750 1755

Ala Ala Gly Gly Thr Cys Thr Cys Ala Cys Ala Cys Cys Ala Gly  
 1760 1765 1770

Gly Cys Thr Gly Gly Gly Gly Ala Cys Cys Ala Cys Thr Gly Gly  
 1775 1780 1785

Cys Thr Cys Ala Thr Cys Cys Gly Cys Gly Gly Ala Cys Cys Cys  
 1790 1795 1800

Cys Thr Gly Gly Ala Gly Thr Ala Thr Gly Thr Gly Cys Cys Ala  
 1805 1810 1815

Thr Cys Thr Gly Cys Cys Ala Ala Ala Gly Thr Gly Gly Ala Gly  
 1820 1825 1830

Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Gly Cys  
 1835 1840 1845

Cys Ala Gly Gly Cys Cys Ala Thr Cys Cys Cys Thr Cys Thr Ala

1850	1855	1860
Gly Ala Cys Gly Ala Gly Ala Ala Cys Gly Ala Gly Gly Gly Cys 1865	1870	1875
Ala Thr Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Thr 1880	1885	1890
Gly Thr Cys Ala Ala Gly Ala Cys Cys Gly Gly Ala Ala Ala Gly 1895	1900	1905
Gly Thr Gly Cys Gly Cys Gly Cys Thr Gly Thr Gly Ala Thr Thr 1910	1915	1920
Gly Gly Ala Ala Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Gly 1925	1930	1935
Cys Thr Gly Ala Cys Cys Cys Ala Gly Gly Ala Cys Gly Ala Ala 1940	1945	1950
Gly Thr Cys Cys Thr Gly Thr Gly Gly Gly Ala Gly Ala Ala Ala 1955	1960	1965
Gly Ala Gly Cys Thr Gly Cys Cys Thr Cys Cys Cys Gly Gly Gly 1970	1975	1980
Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Thr Gly Cys Thr Gly 1985	1990	1995
Ala Ala Cys Ala Ala Gly Gly Gly Gly Cys Ala Gly Gly Ala Cys 2000	2005	2010
Cys Cys Thr Cys Thr Gly Gly Cys Ala Gly Ala Cys Ala Gly Gly 2015	2020	2025
Gly Gly Thr Gly Ala Gly Ala Ala Gly Gly Ala Cys Ala Cys Ala 2030	2035	2040
Gly Cys Thr Ala Ala Gly Ala Gly Cys Cys Thr Cys Cys Ala Gly 2045	2050	2055
Cys Cys Cys Thr Thr Gly Gly Cys Gly Cys Cys Cys Cys Gly Gly 2060	2065	2070

Ala Ala Cys Ala Ala Gly Ala Cys Cys Cys Gly Thr Gly Thr Gly		
2075	2080	2085
Gly Thr Cys Ala Gly Cys Thr Ala Cys Cys Gly Cys Gly Thr Gly		
2090	2095	2100
Cys Cys Cys Cys Ala Cys Ala Ala Cys Gly Cys Thr Gly Cys Gly		
2105	2110	2115
Gly Thr Gly Cys Ala Gly Gly Thr Gly Thr Ala Cys Gly Ala Cys		
2120	2125	2130
Thr Ala Cys Cys Gly Ala Gly Ala Gly Ala Ala Gly Cys Gly Ala		
2135	2140	2145
Gly Cys Cys Cys Gly Cys Gly Thr Gly Gly Thr Cys Thr Thr Cys		
2150	2155	2160
Gly Gly Gly Cys Cys Thr Gly Ala Gly Cys Thr Gly Gly Thr Gly		
2165	2170	2175
Thr Cys Gly Cys Thr Gly Gly Gly Thr Cys Cys Thr Gly Ala Gly		
2180	2185	2190
Gly Ala Gly Cys Ala Gly Thr Thr Cys Ala Cys Ala Gly Thr Gly		
2195	2200	2205
Thr Thr Gly Thr Cys Cys Cys Thr Cys Thr Cys Ala Gly Cys Thr		
2210	2215	2220
Gly Gly Gly Cys Gly Gly Cys Cys Cys Ala Ala Gly Cys Gly Thr		
2225	2230	2235
Cys Cys Cys Cys Ala Thr Gly Cys Cys Cys Gly Cys Cys Gly Thr		
2240	2245	2250
Gly Cys Gly Cys Thr Cys Thr Gly Cys Cys Thr Gly Cys Thr Gly		
2255	2260	2265
Cys Thr Gly Gly Gly Gly Cys Cys Thr Gly Ala Cys Thr Thr Cys		
2270	2275	2280
Thr Thr Cys Ala Cys Ala Gly Ala Cys Gly Thr Cys Ala Thr Cys		
2285	2290	2295

Ala Cys Cys Ala Thr Cys Gly Ala Ala Ala Cys Gly Gly Cys Gly  
 2300 2305 2310

Gly Ala Thr Cys Ala Thr Gly Cys Cys Ala Gly Gly Cys Thr Gly  
 2315 2320 2325

Cys Ala Ala Cys Thr Gly Cys Ala Gly Cys Thr Gly Gly Cys Cys  
 2330 2335 2340

Thr Ala Cys Ala Ala Cys Thr Gly Gly Cys Ala Cys Thr Thr Thr  
 2345 2350 2355

Gly Ala Gly Gly Thr Gly Ala Ala Thr Gly Ala Cys Cys Gly Gly  
 2360 2365 2370

Ala Ala Gly Gly Ala Cys Cys Cys Cys Cys Ala Ala Gly Ala Gly  
 2375 2380 2385

Ala Cys Gly Gly Cys Cys Ala Ala Gly Cys Thr Cys Thr Thr Thr  
 2390 2395 2400

Thr Cys Ala Gly Thr Gly Cys Cys Ala Gly Ala Cys Thr Thr Thr  
 2405 2410 2415

Gly Thr Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Thr Gly Cys  
 2420 2425 2430

Ala Ala Ala Gly Cys Cys Ala Thr Cys Gly Cys Ala Thr Cys Cys  
 2435 2440 2445

Cys Gly Gly Gly Thr Gly Cys Gly Gly Gly Gly Gly Gly Cys Cys  
 2450 2455 2460

Gly Thr Gly Gly Cys Cys Thr Cys Thr Gly Thr Cys Ala Cys Thr  
 2465 2470 2475

Thr Thr Cys Gly Ala Thr Gly Ala Cys Thr Thr Cys Cys Ala Thr  
 2480 2485 2490

Ala Ala Gly Ala Ala Cys Thr Cys Ala Gly Cys Cys Cys Gly Cys  
 2495 2500 2505

Ala Thr Cys Ala Thr Thr Cys Gly Cys Ala Cys Thr Gly Cys Thr

2510		2515		2520
Gly Thr Cys Thr Thr Thr Gly	Gly Cys Thr Thr Thr	Gly Ala Gly		
2525	2530	2535		
Ala Cys Cys Thr Cys Gly Gly	Ala Ala Gly Cys Gly	Ala Ala Gly		
2540	2545	2550		
Gly Gly Cys Cys Cys Cys Gly	Ala Thr Gly Gly Cys	Ala Thr Gly		
2555	2560	2565		
Gly Cys Cys Cys Thr Gly Cys	Cys Cys Ala Gly Gly	Cys Cys Cys		
2570	2575	2580		
Cys Gly Gly Gly Ala Cys Cys	Ala Gly Gly Cys Thr	Gly Thr Cys		
2585	2590	2595		
Thr Thr Cys Cys Cys Cys Cys	Ala Ala Ala Ala Cys	Gly Gly Gly		
2600	2605	2610		
Cys Thr Gly Gly Thr Gly Gly	Thr Cys Ala Gly Cys	Ala Gly Thr		
2615	2620	2625		
Gly Thr Gly Gly Ala Cys Gly	Thr Gly Cys Ala Gly	Thr Cys Ala		
2630	2635	2640		
Gly Thr Gly Gly Ala Gly Cys	Cys Thr Gly Thr Gly	Gly Ala Thr		
2645	2650	2655		
Cys Ala Gly Ala Gly Gly Ala	Cys Cys Cys Gly Gly	Gly Ala Cys		
2660	2665	2670		
Gly Cys Cys Cys Thr Gly Cys	Ala Ala Cys Gly Cys	Ala Gly Cys		
2675	2680	2685		
Gly Thr Cys Cys Ala Gly Cys	Thr Gly Gly Cys Cys	Ala Thr Cys		
2690	2695	2700		
Gly Ala Gly Ala Thr Cys Ala	Cys Cys Ala Cys Cys	Ala Ala Cys		
2705	2710	2715		
Thr Cys Cys Cys Ala Gly Gly	Ala Ala Gly Cys Gly	Gly Cys Gly		
2720	2725	2730		

Gly Cys Cys Ala Ala Gly Cys Ala Thr Gly Ala Gly Gly Cys Thr  
2735 2740 2745

Cys Ala Gly Ala Gly Ala Cys Thr Gly Gly Ala Gly Cys Ala Gly  
2750 2755 2760

Gly Ala Ala Gly Cys Cys Cys Gly Cys Gly Gly Cys Cys Gly Gly  
2765 2770 2775

Cys Thr Thr Gly Ala Gly Cys Gly Gly Cys Ala Gly Ala Ala Gly  
2780 2785 2790

Ala Thr Cys Cys Thr Gly Gly Ala Cys Cys Ala Gly Thr Cys Ala  
2795 2800 2805

Gly Ala Ala Gly Cys Cys Gly Ala Gly Ala Ala Ala Gly Cys Thr  
2810 2815 2820

Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Thr Thr Thr Thr Gly  
2825 2830 2835

Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Cys Thr Cys Thr Gly  
2840 2845 2850

Ala Gly Cys Ala Thr Gly Gly Cys Cys Gly Thr Gly Gly Ala Gly  
2855 2860 2865

Ala Gly Cys Ala Cys Cys Gly Gly Gly Gly Ala Cys Thr Gly Cys Cys  
2870 2875 2880

Ala Ala Gly Gly Cys Gly Gly Ala Gly Gly Cys Cys Gly Ala Gly  
2885 2890 2895

Thr Cys Cys Cys Gly Thr Gly Cys Gly Gly Ala Gly Gly Cys Ala  
2900 2905 2910

Gly Cys Cys Cys Gly Gly Ala Thr Thr Gly Ala Gly Gly Gly Ala  
2915 2920 2925

Gly Ala Ala Gly Gly Gly Thr Cys Cys Gly Thr Gly Cys Thr Gly  
2930 2935 2940

Cys Ala Gly Gly Cys Cys Ala Ala Gly Cys Thr Ala Ala Ala Ala  
2945 2950 2955

Gly Cys Ala Cys Ala Gly Gly Cys Cys Thr Thr Gly Gly Cys Cys  
 2960 2965 2970

Ala Thr Thr Gly Ala Ala Ala Cys Gly Gly Ala Gly Gly Cys Thr  
 2975 2980 2985

Gly Ala Gly Cys Thr Cys Cys Ala Gly Ala Gly Gly Gly Thr Cys  
 2990 2995 3000

Cys Ala Gly Ala Ala Gly Gly Thr Cys Cys Gly Ala Gly Ala Gly  
 3005 3010 3015

Cys Thr Gly Gly Ala Ala Cys Thr Gly Gly Thr Cys Thr Ala Thr  
 3020 3025 3030

Gly Cys Cys Cys Gly Gly Gly Cys Cys Cys Ala Gly Cys Thr Gly  
 3035 3040 3045

Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Thr Gly Ala Gly Cys  
 3050 3055 3060

Ala Ala Gly Gly Cys Thr Cys Ala Gly Cys Ala Gly Cys Thr Gly  
 3065 3070 3075

Gly Cys Thr Gly Ala Gly Gly Thr Gly Gly Ala Gly Gly Thr Gly  
 3080 3085 3090

Ala Ala Gly Ala Ala Gly Thr Thr Cys Ala Ala Gly Cys Ala Gly  
 3095 3100 3105

Ala Thr Gly Ala Cys Ala Gly Ala Gly Gly Cys Cys Ala Thr Ala  
 3110 3115 3120

Gly Gly Cys Cys Cys Cys Ala Gly Cys Ala Cys Cys Ala Thr Cys  
 3125 3130 3135

Ala Gly Gly Gly Ala Cys Cys Thr Thr Gly Cys Thr Gly Thr Gly  
 3140 3145 3150

Gly Cys Thr Gly Gly Gly Cys Cys Thr Gly Ala Gly Ala Thr Gly  
 3155 3160 3165

Cys Ala Gly Gly Thr Ala Ala Ala Ala Cys Thr Gly Cys Thr Cys



3170	3175	3180
Cys Ala Gly Thr Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly		
3185	3190	3195
Ala Ala Ala Thr Cys Ala Ala Cys Cys Cys Thr Cys Ala Thr Cys		
3200	3205	3210
Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr Cys Cys Ala Cys Thr		
3215	3220	3225
Cys Cys Cys Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Thr Cys		
3230	3235	3240
Ala Ala Cys Ala Cys Ala Gly Cys Cys Thr Thr Thr Gly Gly Gly		
3245	3250	3255
Cys Thr Gly Cys Thr Gly Gly Gly Gly Ala Thr Gly Gly Gly Gly		
3260	3265	3270
Cys Cys Cys Gly Ala Gly Gly Gly Thr Cys Ala Gly Cys Cys Cys		
3275	3280	3285
Cys Thr Gly Gly Gly Cys Ala Gly Ala Ala Gly Gly Gly Thr Gly		
3290	3295	3300
Gly Cys Cys Ala Gly Thr Gly Gly Gly Cys Cys Cys Ala Gly Cys		
3305	3310	3315
Cys Cys Thr Gly Gly Gly Gly Ala Gly Gly Gly Gly Ala Thr Ala		
3320	3325	3330
Thr Cys Cys Cys Cys Cys Cys Ala Gly Thr Cys Thr Gly Cys Thr		
3335	3340	3345
Cys Ala Gly Gly Cys Cys Cys Cys Thr Cys Ala Ala Gly Cys Thr		
3350	3355	3360
Cys Cys Thr Gly Gly Ala Gly Ala Cys Ala Ala Cys Cys Ala Cys		
3365	3370	3375
Gly Thr Gly Gly Thr Gly Cys Cys Thr Gly Thr Ala Cys Thr Gly		
3380	3385	3390

Cys Gly Cys Thr Ala Ala  
3395

<210> 48  
<211> 1100  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> synthesized and Rattus norvegicus

<400> 48

Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val  
1 5 10 15

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Met  
 225 230 235 240

Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile His  
 245 250 255

Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro Lys  
 260 265 270

Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val Arg  
 275 280 285

Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro Val  
 290 295 300

Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln Val  
 305 310 315 320

Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro Phe  
 325 330 335

Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu Gln  
 340 345 350

Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp Phe  
 355 360 365

Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu Phe  
 370 375 380

Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val Glu  
 385 390 395 400

Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu Arg  
 405 410 415

Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr Gly  
 420 425 430

Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val Phe  
 435 440 445

Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys Thr  
 450 455 460

Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly Val  
 465 470 475 480

Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr Glu  
 485 490 495

Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro Ile  
 500 505 510

Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met Gly  
 515 520 525

Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly Glu  
 530 535 540

Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile Gln  
 545 550 555 560

Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala Leu  
 565 570 575

Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln Ala  
 580 585 590

Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser Ala  
 595 600 605

Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln Asn  
 610 615 620

Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala Val  
 625 630 635 640

Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu Lys

645	650	655
Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp Pro		
660	665	670
Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro Ser		
675	680	685
Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His Asn		
690	695	700
Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val Val		
705	710	715
Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr Val		
725	730	735
Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg Ala		
740	745	750
Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr Ile		
755	760	765
Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn Trp		
770	775	780
His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys Leu		
785	790	795
Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala Ser		
805	810	815
Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His Lys		
820	825	830
Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met Ser		
835	840	845
Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp Gln		
850	855	860
Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val Gln		
865	870	875
		880

146/429

<210> 49  
 <211> 3303  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Rattus norvegicus

<400> 49

Ala Thr Gly Ala Gly Cys Ala Ala Gly Gly Gly Cys Gly Ala Gly Gly  
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Ala Ala Cys Thr Gly Thr Thr Cys Ala Cys Thr Gly Gly Cys Gly Thr  
 20 25 30

Gly Gly Thr Cys Cys Cys Ala Ala Thr Thr Cys Thr Cys Gly Thr Gly  
 35 40 45

Gly Ala Ala Cys Thr Gly Gly Ala Thr Gly Gly Cys Gly Ala Thr Gly  
 50 55 60

Thr Gly Ala Ala Thr Gly Gly Gly Cys Ala Cys Ala Ala Ala Thr Thr  
 65 70 75 80

Thr Thr Cys Thr Gly Thr Cys Ala Gly Cys Gly Gly Ala Gly Ala Gly  
 85 90 95

Gly Gly Thr Gly Ala Ala Gly Gly Thr Gly Ala Thr Gly Cys Cys Ala  
 100 105 110

Cys Ala Thr Ala Cys Gly Gly Ala Ala Ala Gly Cys Thr Cys Ala Cys  
 115 120 125

Cys Cys Thr Gly Ala Ala Ala Thr Thr Cys Ala Thr Cys Thr Gly Cys  
 130 135 140

Ala Cys Cys Ala Cys Thr Gly Gly Ala Ala Ala Gly Cys Thr Cys Cys  
 145 150 155 160

Cys Thr Gly Thr Gly Cys Cys Ala Thr Gly Gly Cys Cys Ala Ala Cys  
 165 170 175

Ala Cys Thr Gly Gly Thr Cys Ala Cys Thr Ala Cys Cys Thr Thr Cys  
 180 185 190

Ala Cys Cys Thr Ala Thr Gly Gly Cys Gly Thr Gly Cys Ala Gly Thr  
 195 200 205

Gly Cys Thr Thr Thr Thr Cys Cys Ala Gly Ala Thr Ala Cys Cys Cys  
 210 215 220

Ala Gly Ala Cys Cys Ala Thr Ala Thr Gly Ala Ala Gly Cys Ala Gly  
 225 230 235 240

Cys Ala Thr Gly Ala Cys Thr Thr Thr Thr Thr Cys Ala Ala Gly Ala  
 245 250 255

Gly Cys Gly Cys Cys Ala Thr Gly Cys Cys Cys Gly Ala Gly Gly Gly  
 260 265 270

Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Gly Ala Gly Ala  
 275 280 285

Ala Cys Cys Ala Thr Cys Thr Thr Thr Thr Thr Cys Ala Ala Ala Gly  
 290 295 300

Ala Thr Gly Ala Cys Gly Gly Gly Ala Ala Cys Thr Ala Cys Ala Ala  
 305 310 315 320

Gly Ala Cys Cys Cys Gly Cys Gly Cys Thr Gly Ala Ala Gly Thr Cys  
 325 330 335

Ala Ala Gly Thr Thr Cys Gly Ala Ala Gly Gly Thr Gly Ala Cys Ala  
 340 345 350

Cys Cys Cys Thr Gly Gly Thr Gly Ala Ala Thr Ala Gly Ala Ala Thr  
 355 360 365

Cys Gly Ala Gly Cys Thr Gly Ala Ala Gly Gly Gly Cys Ala Thr Thr  
 370 375 380

Gly Ala Cys Thr Thr Thr Ala Ala Gly Gly Ala Gly Gly Ala Thr Gly  
 385 390 395 400

Gly Ala Ala Ala Cys Ala Thr Thr Cys Thr Cys Gly Gly Cys Cys Ala  
 405 410 415

Cys Ala Ala Gly Cys Thr Gly Gly Ala Ala Thr Ala Cys Ala Ala Cys  
 420 425 430



Thr Ala Thr Ala Ala Cys Thr Cys Cys Cys Ala Cys Ala Ala Thr Gly  
 435 440 445

Thr Gly Thr Ala Cys Ala Thr Cys Ala Thr Gly Gly Cys Cys Gly Ala  
 450 455 460

Cys Ala Ala Gly Cys Ala Ala Ala Ala Gly Ala Ala Thr Gly Gly Cys  
 465 470 475 480

Ala Thr Cys Ala Ala Gly Gly Thr Cys Ala Ala Cys Thr Thr Cys Ala  
 485 490 495

Ala Gly Ala Thr Cys Ala Gly Ala Cys Ala Cys Ala Ala Cys Ala Thr  
 500 505 510

Thr Gly Ala Gly Gly Ala Thr Gly Gly Ala Thr Cys Cys Gly Thr Gly  
 515 520 525

Cys Ala Gly Cys Thr Gly Gly Cys Cys Gly Ala Cys Cys Ala Thr Thr  
 530 535 540

Ala Thr Cys Ala Ala Cys Ala Gly Ala Ala Cys Ala Cys Thr Cys Cys  
 545 550 555 560

Ala Ala Thr Cys Gly Gly Cys Gly Ala Cys Gly Gly Cys Cys Cys Thr  
 565 570 575

Gly Thr Gly Cys Thr Cys Cys Thr Cys Cys Cys Ala Gly Ala Cys Ala  
 580 585 590

Ala Cys Cys Ala Thr Thr Ala Cys Cys Thr Gly Thr Cys Cys Ala Cys  
 595 600 605

Cys Cys Ala Gly Thr Cys Thr Gly Cys Cys Cys Thr Gly Thr Cys Thr  
 610 615 620

Ala Ala Ala Gly Ala Thr Cys Cys Cys Ala Ala Cys Gly Ala Ala Ala  
 625 630 635 640

Ala Gly Ala Gly Ala Gly Ala Cys Cys Ala Cys Ala Thr Gly Gly Thr  
 645 650 655

Cys Cys Thr Gly Cys Thr Gly Gly Ala Gly Thr Thr Thr Gly Thr Gly

660	665	670
Ala Cys Cys Gly Cys Thr Gly Cys Thr Gly Gly Gly Ala Thr Cys Ala 675 680 685		
Cys Ala Cys Ala Thr Gly Gly Cys Ala Thr Gly Gly Ala Cys Gly Ala 690 695 700		
Gly Cys Thr Gly Thr Ala Cys Ala Ala Gly Cys Cys Cys Ala Thr Gly 705 710 715 720		
Gly Cys Ala Ala Cys Thr Gly Ala Ala Gly Ala Gly Gly Cys Cys Ala 725 730 735		
Thr Cys Ala Thr Cys Cys Gly Cys Ala Thr Cys Cys Cys Cys Cys Cys 740 745 750		
Ala Thr Ala Cys Cys Ala Cys Thr Ala Cys Ala Thr Cys Cys Ala Thr 755 760 765		
Gly Thr Gly Cys Thr Gly Gly Ala Cys Cys Ala Gly Ala Ala Cys Ala 770 775 780		
Gly Thr Ala Ala Thr Gly Thr Gly Thr Cys Cys Cys Gly Thr Gly Thr 785 790 795 800		
Gly Gly Ala Gly Gly Thr Thr Gly Gly Ala Cys Cys Ala Ala Ala Gly 805 810 815		
Ala Cys Cys Thr Ala Cys Ala Thr Cys Cys Gly Gly Cys Ala Gly Gly 820 825 830		
Ala Cys Ala Ala Thr Gly Ala Gly Ala Gly Gly Gly Thr Ala Cys Thr 835 840 845		
Gly Thr Thr Thr Gly Cys Cys Cys Cys Ala Gly Thr Thr Cys Gly Cys 850 855 860		
Ala Thr Gly Gly Thr Gly Ala Cys Cys Gly Thr Cys Cys Cys Cys Cys 865 870 875 880		
Cys Ala Cys Gly Cys Cys Ala Cys Thr Ala Cys Thr Gly Cys Ala Thr 885 890 895		

Ala Gly Thr Gly Gly Cys Cys Ala Ala Cys Cys Cys Thr Gly Thr Gly  
 900 905 910

Thr Cys Cys Cys Gly Gly Gly Ala Cys Ala Cys Cys Cys Ala Gly Ala  
 915 920 925

Gly Thr Thr Cys Thr Gly Thr Gly Thr Thr Ala Thr Thr Thr Gly Ala  
 930 935 940

Cys Ala Thr Cys Ala Cys Ala Gly Gly Ala Cys Ala Ala Gly Thr Cys  
 945 950 955 960

Cys Gly Ala Cys Thr Cys Cys Gly Gly Cys Ala Cys Gly Cys Thr Gly  
 965 970 975

Ala Cys Cys Ala Gly Gly Ala Gly Ala Thr Cys Cys Gly Ala Cys Thr  
 980 985 990

Ala Gly Cys Cys Cys Ala Gly Gly Ala Cys Cys Cys Cys Thr Thr Cys  
 995 1000 1005

Cys Cys Cys Cys Thr Gly Thr Ala Thr Cys Cys Ala Gly Gly Gly  
 1010 1015 1020

Gly Ala Gly Gly Thr Gly Cys Thr Gly Gly Ala Ala Ala Ala Gly  
 1025 1030 1035

Gly Ala Cys Ala Thr Cys Ala Cys Cys Cys Cys Ala Cys Thr Gly  
 1040 1045 1050

Cys Ala Gly Gly Thr Gly Gly Thr Thr Cys Thr Gly Cys Cys Cys  
 1055 1060 1065

Ala Ala Cys Ala Cys Ala Gly Cys Ala Cys Thr Gly Cys Ala Thr  
 1070 1075 1080

Cys Thr Thr Ala Ala Gly Gly Cys Gly Thr Thr Gly Cys Thr Gly  
 1085 1090 1095

Gly Ala Cys Thr Thr Thr Gly Ala Gly Gly Ala Thr Ala Ala Gly  
 1100 1105 1110

Ala Ala Thr Gly Gly Ala Gly Ala Cys Ala Ala Gly Gly Thr Cys  
 1115 1120 1125

Ala Thr Gly Gly Cys Ala Gly Gly Ala Gly Ala Cys Gly Ala Gly  
 1130 1135 1140  
 Thr Gly Gly Cys Thr Ala Thr Thr Thr Gly Ala Gly Gly Gly Ala  
 1145 1150 1155  
 Cys Cys Thr Gly Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Cys  
 1160 1165 1170  
 Cys Cys Ala Cys Ala Gly Ala Ala Gly Gly Ala Ala Gly Thr Gly  
 1175 1180 1185  
 Gly Ala Ala Gly Thr Cys Gly Thr Gly Gly Ala Gly Ala Thr Cys  
 1190 1195 1200  
 Ala Thr Thr Cys Ala Gly Gly Cys Cys Ala Cys Ala Gly Thr Cys  
 1205 1210 1215  
 Ala Thr Cys Ala Ala Ala Cys Ala Gly Ala Ala Cys Cys Ala Ala  
 1220 1225 1230  
 Gly Cys Ala Cys Thr Gly Cys Gly Gly Cys Thr Ala Ala Gly Gly  
 1235 1240 1245  
 Gly Cys Cys Cys Gly Ala Ala Ala Gly Gly Ala Gly Thr Gly Cys  
 1250 1255 1260  
 Thr Thr Thr Gly Ala Cys Cys Gly Gly Gly Ala Gly Gly Gly Cys  
 1265 1270 1275  
 Ala Ala Gly Gly Gly Gly Cys Gly Cys Gly Thr Gly Ala Cys Ala  
 1280 1285 1290  
 Gly Gly Thr Gly Ala Gly Gly Ala Gly Thr Gly Gly Cys Thr Gly  
 1295 1300 1305  
 Gly Thr Cys Cys Gly Ala Thr Cys Cys Gly Thr Gly Gly Gly Gly  
 1310 1315 1320  
 Gly Cys Thr Thr Ala Cys Cys Thr Cys Cys Cys Ala Gly Cys Thr  
 1325 1330 1335  
 Gly Thr Cys Thr Thr Thr Gly Ala Ala Gly Ala Gly Gly Thr Gly

1340		1345		1350
Cys Thr Gly Gly Ala Thr	Cys Thr Gly Gly Thr	Gly Gly Ala Thr		
1355	1360	1365		
Gly Cys Thr Gly Thr Gly	Ala Thr Cys Cys Thr	Thr Ala Cys Ala		
1370	1375	1380		
Gly Ala Ala Ala Ala Gly	Ala Cys Thr Gly Cys	Cys Cys Thr Gly		
1385	1390	1395		
Cys Ala Cys Cys Thr Cys	Cys Gly Gly Gly Cys	Thr Cys Thr Gly		
1400	1405	1410		
Cys Ala Gly Ala Ala Cys	Thr Thr Cys Ala Gly	Gly Gly Ala Cys		
1415	1420	1425		
Cys Thr Thr Cys Gly Gly	Gly Gly Ala Gly Thr	Gly Cys Thr Cys		
1430	1435	1440		
Cys Ala Cys Cys Gly Cys	Ala Cys Cys Gly Gly	Gly Gly Ala Gly		
1445	1450	1455		
Gly Ala Ala Thr Gly Gly	Thr Thr Ala Gly Thr	Gly Ala Cys Ala		
1460	1465	1470		
Gly Thr Gly Cys Ala Gly	Gly Ala Cys Ala Cys	Ala Gly Ala Ala		
1475	1480	1485		
Gly Cys Cys Cys Ala Thr	Gly Thr Thr Cys Cys	Ala Gly Ala Thr		
1490	1495	1500		
Gly Thr Cys Thr Ala Thr	Gly Ala Gly Gly Ala	Gly Gly Thr Gly		
1505	1510	1515		
Cys Thr Thr Gly Gly Gly	Gly Thr Ala Gly Thr	Ala Cys Cys Cys		
1520	1525	1530		
Ala Thr Cys Ala Cys Cys	Ala Cys Cys Cys Thr	Gly Gly Gly Ala		
1535	1540	1545		
Cys Cys Thr Cys Gly Ala	Cys Ala Cys Thr Ala	Cys Thr Gly Thr		
1550	1555	1560		

Gly Thr Cys Ala Thr Thr Cys Thr Thr Gly Ala Cys Cys Cys Ala  
 1565 1570 1575

Ala Thr Gly Gly Gly Ala Cys Cys Ala Gly Ala Cys Gly Gly Cys  
 1580 1585 1590

Ala Ala Gly Ala Ala Cys Cys Ala Gly Cys Thr Gly Gly Gly Ala  
 1595 1600 1605

Cys Ala Ala Ala Ala Gly Cys Gly Thr Gly Thr Thr Gly Thr Cys  
 1610 1615 1620

Ala Ala Gly Gly Gly Ala Gly Ala Gly Ala Ala Gly Thr Cys Cys  
 1625 1630 1635

Thr Thr Thr Thr Thr Cys Cys Thr Cys Cys Ala Gly Cys Cys Ala  
 1640 1645 1650

Gly Gly Ala Gly Ala Gly Ala Gly Gly Cys Thr Gly Gly Ala Gly  
 1655 1660 1665

Cys Gly Ala Gly Gly Cys Ala Thr Cys Cys Ala Gly Gly Ala Thr  
 1670 1675 1680

Gly Thr Gly Thr Ala Thr Gly Thr Gly Cys Thr Gly Thr Cys Ala  
 1685 1690 1695

Gly Ala Gly Cys Ala Gly Cys Ala Gly Gly Gly Gly Cys Thr Gly  
 1700 1705 1710

Cys Thr Ala Cys Thr Gly Ala Ala Gly Gly Cys Ala Cys Thr Gly  
 1715 1720 1725

Cys Ala Gly Cys Cys Cys Cys Thr Gly Gly Ala Gly Gly Ala Gly  
 1730 1735 1740

Gly Gly Ala Gly Ala Gly Ala Gly Cys Gly Ala Gly Gly Ala Gly  
 1745 1750 1755

Ala Ala Gly Gly Thr Cys Thr Cys Cys Cys Ala Thr Cys Ala Gly  
 1760 1765 1770

Gly Cys Cys Gly Gly Ala Gly Ala Cys Thr Gly Cys Thr Gly Gly  
 1775 1780 1785

Cys Thr Cys Ala Thr Cys Cys Gly Thr Gly Gly Gly Cys Cys Cys  
 1790 1795 1800

Cys Thr Gly Gly Ala Gly Thr Ala Thr Gly Thr Gly Cys Cys Ala  
 1805 1810 1815

Thr Cys Thr Gly Cys Ala Ala Ala Ala Gly Thr Gly Gly Ala Gly  
 1820 1825 1830

Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Gly Thr  
 1835 1840 1845

Cys Ala Gly Gly Cys Thr Ala Thr Cys Cys Cys Thr Cys Thr Gly  
 1850 1855 1860

Gly Ala Cys Cys Ala Ala Ala Ala Thr Gly Ala Gly Gly Gly Cys  
 1865 1870 1875

Ala Thr Cys Thr Ala Thr Gly Thr Gly Cys Ala Gly Gly Ala Thr  
 1880 1885 1890

Gly Thr Cys Ala Ala Gly Ala Cys Gly Gly Gly Gly Ala Ala Gly  
 1895 1900 1905

Gly Thr Gly Cys Gly Gly Gly Cys Thr Gly Thr Gly Ala Thr Thr  
 1910 1915 1920

Gly Gly Ala Ala Gly Cys Ala Cys Cys Thr Ala Cys Ala Thr Gly  
 1925 1930 1935

Cys Thr Gly Ala Cys Thr Cys Ala Gly Gly Ala Thr Gly Ala Ala  
 1940 1945 1950

Gly Thr Cys Cys Thr Gly Thr Gly Gly Gly Ala Ala Ala Ala Gly  
 1955 1960 1965

Gly Ala Gly Cys Thr Gly Cys Cys Thr Thr Cys Thr Gly Gly Gly  
 1970 1975 1980

Gly Thr Gly Gly Ala Gly Gly Ala Gly Cys Thr Gly Cys Thr Gly  
 1985 1990 1995

Ala Ala Cys Thr Thr Gly Gly Gly Gly Cys Ala Thr Gly Ala Cys

2000	2005	2010
Cys Cys Thr Cys Thr Gly Gly 2015	Cys Ala Gly Ala Cys 2020	Cys Ala Gly Gly 2025
Gly Gly Thr Cys Ala Gly Ala 2030	Ala Gly Gly Gly Cys 2035	Ala Cys Ala 2040
Gly Cys Cys Ala Ala Gly Cys 2045	Cys Cys Cys Thr Thr 2050	Cys Ala Gly 2055
Cys Cys Cys Thr Cys Ala Gly 2060	Cys Thr Cys Cys Ala 2065	Ala Gly Gly 2070
Ala Ala Cys Ala Ala Gly Ala 2075	Cys Cys Cys Gly Ala 2080	Gly Thr Gly 2085
Gly Thr Cys Ala Gly Cys Thr 2090	Ala Cys Cys Gly Thr 2095	Gly Thr Cys 2100
Cys Cys Gly Cys Ala Cys Ala 2105	Ala Thr Gly Cys Ala 2110	Gly Cys Gly 2115
Gly Thr Gly Cys Ala Gly Gly 2120	Thr Cys Thr Ala Thr 2125	Gly Ala Cys 2130
Thr Ala Cys Ala Gly Ala Gly 2135	Cys Cys Ala Ala Gly 2140	Ala Gly Ala 2145
Gly Cys Cys Cys Gly Thr Gly 2150	Thr Gly Gly Thr Cys 2155	Thr Thr Thr 2160
Gly Gly Gly Cys Cys Cys Gly 2165	Ala Gly Cys Thr Ala 2170	Gly Thr Gly 2175
Ala Cys Ala Cys Thr Gly Gly 2180	Ala Thr Cys Cys Thr 2185	Gly Ala Gly 2190
Gly Ala Gly Cys Ala Gly Thr 2195	Thr Cys Ala Cys Ala 2200	Gly Thr Ala 2205
Thr Thr Gly Thr Cys Cys Cys 2210	Thr Thr Thr Cys Thr 2215	Gly Cys Cys 2220



Gly Gly Gly Cys Gly Ala Cys Cys Cys Ala Ala Gly Cys Gly Thr  
 2225 2230 2235

Cys Cys Thr Cys Ala Thr Gly Cys Cys Cys Gly Cys Cys Gly Thr  
 2240 2245 2250

Gly Cys Ala Cys Thr Cys Thr Gly Cys Cys Thr Ala Cys Thr Gly  
 2255 2260 2265

Cys Thr Gly Gly Gly Ala Cys Cys Thr Gly Ala Thr Thr Thr Cys  
 2270 2275 2280

Thr Thr Thr Ala Cys Thr Gly Ala Thr Gly Thr Cys Ala Thr Cys  
 2285 2290 2295

Ala Cys Cys Ala Thr Cys Gly Ala Ala Ala Cys Thr Gly Cys Ala  
 2300 2305 2310

Gly Ala Thr Cys Ala Thr Gly Cys Cys Ala Gly Gly Thr Thr Gly  
 2315 2320 2325

Cys Ala Gly Cys Thr Gly Cys Ala Gly Cys Thr Thr Gly Cys Cys  
 2330 2335 2340

Thr Ala Cys Ala Ala Cys Thr Gly Gly Cys Ala Cys Thr Thr Thr  
 2345 2350 2355

Gly Ala Ala Cys Thr Gly Ala Ala Gly Ala Ala Cys Cys Gly Gly  
 2360 2365 2370

Ala Ala Thr Gly Ala Cys Cys Cys Thr Gly Cys Ala Gly Ala Gly  
 2375 2380 2385

Gly Cys Ala Gly Cys Cys Ala Ala Gly Cys Thr Thr Thr Thr Cys  
 2390 2395 2400

Thr Cys Cys Gly Thr Gly Cys Cys Thr Gly Ala Cys Thr Thr Cys  
 2405 2410 2415

Gly Thr Gly Gly Gly Thr Gly Ala Cys Gly Cys Cys Thr Gly Cys  
 2420 2425 2430

Ala Ala Gly Gly Cys Cys Ala Thr Thr Gly Cys Ala Thr Cys Cys  
 2435 2440 2445

Cys Gly	Ala Gly Thr Cys Cys	Gly Gly Gly Gly Gly	Gly Cys Thr
2450		2455	2460
Gly Thr	Ala Gly Cys Cys Thr	Cys Thr Gly Thr Cys	Ala Cys Cys
2465		2470	2475
Thr Thr	Thr Gly Ala Thr Gly	Ala Cys Thr Thr Cys	Cys Ala Thr
2480		2485	2490
Ala Ala	Ala Ala Ala Cys Thr	Cys Ala Gly Cys Cys	Cys Gly Gly
2495		2500	2505
Ala Thr	Cys Ala Thr Thr Cys	Gly Ala Ala Thr Gly	Gly Cys Thr
2510		2515	2520
Gly Thr	Thr Thr Thr Thr Gly	Gly Cys Thr Thr Thr	Gly Ala Gly
2525		2530	2535
Ala Thr	Gly Thr Cys Thr Gly	Ala Ala Gly Ala Cys	Ala Cys Ala
2540		2545	2550
Gly Gly	Thr Cys Cys Thr Gly	Ala Thr Gly Gly Cys	Ala Cys Ala
2555		2560	2565
Cys Thr	Cys Cys Thr Gly Cys	Cys Cys Ala Ala Gly	Gly Cys Thr
2570		2575	2580
Cys Gly	Ala Gly Ala Cys Cys	Ala Gly Gly Cys Ala	Gly Thr Cys
2585		2590	2595
Thr Thr	Thr Cys Cys Cys Cys	Ala Ala Ala Ala Cys	Gly Gly Gly
2600		2605	2610
Cys Thr	Gly Gly Thr Ala Gly	Thr Cys Ala Gly Cys	Ala Gly Thr
2615		2620	2625
Gly Thr	Gly Gly Ala Thr Gly	Thr Gly Cys Ala Gly	Thr Cys Ala
2630		2635	2640
Gly Thr	Gly Gly Ala Gly Cys	Cys Cys Gly Thr Gly	Gly Ala Cys
2645		2650	2655
Cys Ala	Gly Ala Gly Gly Ala	Cys Cys Cys Gly Gly	Gly Ala Thr

2660		2665		2670
Gly Cys Cys Cys Thr Thr Cys Ala Gly Cys Gly Cys Ala Gly Cys				
2675		2680		2685
Gly Thr Thr Cys Ala Gly Cys Thr Gly Gly Cys Cys Ala Thr Cys				
2690		2695		2700
Gly Ala Ala Ala Thr Thr Ala Cys Cys Ala Cys Cys Ala Ala Cys				
2705		2710		2715
Thr Cys Cys Cys Ala Gly Gly Ala Gly Gly Cys Ala Gly Cys Ala				
2720		2725		2730
Gly Cys Cys Ala Ala Gly Cys Ala Cys Gly Ala Gly Gly Cys Thr				
2735		2740		2745
Cys Ala Gly Ala Gly Ala Cys Thr Gly Gly Ala Ala Cys Ala Gly				
2750		2755		2760
Gly Ala Ala Gly Cys Cys Cys Gly Thr Gly Gly Thr Cys Gly Gly				
2765		2770		2775
Cys Thr Thr Gly Ala Gly Ala Gly Gly Cys Ala Gly Ala Ala Gly				
2780		2785		2790
Ala Thr Cys Thr Thr Gly Gly Ala Cys Cys Ala Gly Thr Cys Ala				
2795		2800		2805
Gly Ala Ala Gly Cys Thr Gly Ala Ala Ala Ala Ala Gly Cys Cys				
2810		2815		2820
Cys Gly Cys Ala Ala Gly Gly Ala Ala Cys Thr Cys Thr Thr Gly				
2825		2830		2835
Gly Ala Gly Cys Thr Thr Gly Ala Gly Gly Cys Thr Ala Thr Gly				
2840		2845		2850
Ala Gly Cys Ala Thr Gly Gly Cys Thr Gly Thr Gly Gly Ala Gly				
2855		2860		2865
Ala Gly Cys Ala Cys Gly Gly Gly Thr Ala Ala Thr Gly Cys Cys				
2870		2875		2880

Ala Ala Ala Gly Cys Ala Gly Ala Gly Gly Cys Thr Gly Ala Gly  
2885 2890 2895

Thr Cys Cys Cys Gly Thr Gly Cys Ala Gly Ala Gly Gly Cys Ala  
2900 2905 2910

Gly Cys Gly Ala Gly Gly Ala Thr Cys Gly Ala Ala Gly Gly Ala  
2915 2920 2925

Gly Ala Ala Gly Gly Cys Thr Cys Thr Gly Thr Gly Cys Thr Gly  
2930 2935 2940

Cys Ala Gly Gly Cys Cys Ala Ala Gly Cys Thr Cys Ala Ala Gly  
2945 2950 2955

Gly Cys Ala Cys Ala Gly Gly Cys Gly Cys Thr Ala Gly Cys Cys  
2960 2965 2970

Ala Thr Thr Gly Ala Gly Ala Cys Gly Gly Ala Gly Gly Cys Thr  
2975 2980 2985

Gly Ala Gly Thr Thr Gly Gly Ala Gly Cys Gly Ala Gly Thr Ala  
2990 2995 3000

Ala Ala Gly Ala Ala Ala Gly Thr Ala Cys Gly Ala Gly Ala Gly  
3005 3010 3015

Ala Thr Gly Gly Ala Ala Cys Thr Gly Ala Thr Cys Thr Ala Thr  
3020 3025 3030

Gly Cys Cys Cys Gly Gly Gly Cys Cys Cys Ala Gly Thr Thr Gly  
3035 3040 3045

Gly Ala Gly Cys Thr Gly Gly Ala Gly Gly Thr Gly Ala Gly Cys  
3050 3055 3060

Ala Ala Gly Gly Cys Gly Cys Ala Gly Cys Ala Gly Cys Thr Thr  
3065 3070 3075

Gly Cys Cys Ala Ala Thr Gly Thr Gly Gly Ala Gly Gly Cys Ala  
3080 3085 3090

Ala Ala Gly Ala Ala Gly Thr Thr Cys Ala Ala Gly Gly Ala Gly  
3095 3100 3105

Ala Thr Gly Ala Cys Ala Gly Ala Gly Gly Cys Ala Cys Thr Gly  
 3110 3115 3120

Gly Gly Cys Cys Cys Cys Gly Gly Cys Ala Cys Cys Ala Thr Cys  
 3125 3130 3135

Ala Gly Gly Gly Ala Cys Cys Thr Gly Gly Cys Thr Gly Thr Gly  
 3140 3145 3150

Gly Cys Cys Gly Gly Gly Cys Cys Ala Gly Ala Gly Ala Thr Gly  
 3155 3160 3165

Cys Ala Gly Gly Thr Gly Ala Ala Ala Cys Thr Thr Cys Thr Cys  
 3170 3175 3180

Cys Ala Gly Thr Cys Cys Cys Thr Gly Gly Gly Cys Cys Thr Gly  
 3185 3190 3195

Ala Ala Ala Thr Cys Cys Ala Cys Thr Cys Thr Cys Ala Thr Cys  
 3200 3205 3210

Ala Cys Cys Gly Ala Thr Gly Gly Cys Thr Cys Gly Thr Cys Thr  
 3215 3220 3225

Cys Cys Cys Ala Thr Cys Ala Ala Cys Cys Thr Cys Thr Thr Cys  
 3230 3235 3240

Ala Gly Cys Ala Cys Ala Gly Cys Cys Thr Thr Cys Gly Gly Gly  
 3245 3250 3255

Thr Thr Gly Cys Thr Gly Gly Gly Gly Cys Thr Gly Gly Gly Gly  
 3260 3265 3270

Thr Cys Thr Gly Ala Thr Gly Gly Thr Cys Ala Gly Cys Cys Gly  
 3275 3280 3285

Cys Cys Ala Gly Cys Ala Cys Ala Gly Ala Ala Gly Thr Gly Ala  
 3290 3295 3300

<210> 50  
 <211> 267  
 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Homo sapiens

&lt;400&gt; 50

Met Ala Gly Cys Gly Cys Pro Cys Gly Cys Gly Ala Gly Ile Pro Ala  
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Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser  
 20 25 30

Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val  
 35 40 45

Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser  
 50 55 60

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe  
 65 70 75 80

Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu  
 85 90 95

Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp  
 100 105 110

Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe  
 115 120 125

Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn  
 130 135 140

Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val  
 145 150 155 160

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val Leu  
 165 170 175

Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys Ser  
 180 185 190

Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala  
 195 200 205

Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu Gly

210	215	220
Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp		
225	230	235 240
Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser		
245	250	255
Pro Leu His Arg Val Leu His Tyr Ser Gln Gly		
260	265	

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 <211> 804  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens

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<210> 52  
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 <212> PRT  
 <213> Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Homo sapiens

&lt;400&gt; 52

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Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys Tyr Leu Pro Gln  
 20 25 30

Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile Lys Glu Asn Gly Gly Lys  
 35 40 45

Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile Ile Leu Asp Asn  
 50 55 60

Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile Gln Lys Asn His  
 65 70 75 80

Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser Ile Arg Glu Lys  
 85 90 95

Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys Pro Leu Asp Ile  
 100 105 110

Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu Val Lys Thr Glu  
 115 120 125

Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp Thr Val Glu Leu  
 130 135 140

Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His Leu Pro Gln Asp  
 145 150 155 160

Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val Gly Met Glu Gly  
 165 170 175

Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser Arg Asp Ser Arg  
 180 185 190

Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu Asp Asp Gly Met  
 195 200 205

Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser Glu Asp Ala Ser



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Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile Leu Cys Arg Gly  
 450 455 460

Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val Gln Arg Thr Asp  
 465 470 475 480

Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp Ser Leu Ser Thr  
 485 490 495

Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly Thr Arg Leu Leu  
 500 505 510

Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp Leu His Glu Lys  
 515 520 525

Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val His Gly  
 530 535 540

Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp Glu Phe  
 545 550 555 560

Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile Lys Phe  
 565 570 575

Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp His Thr  
 580 585 590

Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser Lys Val Glu  
 595 600 605

Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser Thr Lys Ala Gly  
 610 615 620

Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu Asp Val His Ile  
 625 630 635 640

Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile Val Phe Gln Thr  
 645 650 655

Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys Tyr Ile Phe Pro  
 660 665 670

Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala Phe Ile Asn Gly  
 675 680 685

Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu Ala Gln Gln Glu  
 690 695 700

Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr Leu Met Ser Gln  
 705 710 715 720

Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn Leu Pro Pro Lys  
 725 730 735

Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu Leu Ser Ile Leu  
 740 745 750

Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val Ala Pro Trp Gln  
 755 760 765

Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr Val Glu Lys Ile  
 770 775 780

Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu Thr Met Ser  
 785 790 795 800

Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser Asp Thr His Glu  
 805 810 815

Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val Ile Ser Thr Met Glu  
 820 825 830

Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His Ile Gly Leu Ser  
 835 840 845

Ala Ala Tyr Leu Pro Arg Met Trp Val Glu Lys His Pro Glu Lys Glu  
 850 855 860

Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp Leu Asp Val Asp Leu  
 865 870 875 880

Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys Leu Asp Cys Ser  
 885 890 895

Ser Ser Met Glu Gly Val Thr Phe Leu Gln Ala Lys Gln Ile Thr Leu  
 900 905 910

His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val Asn Ile Ile Gln

915	920	925
Phe Gly Thr Gly Tyr Lys Glu Leu Phe Ser Tyr Pro Lys His Ile Thr 930 935 940		
Ser Asn Thr Thr Ala Ala Glu Phe Ile Met Ser Ala Thr Pro Thr Met 945 950 955 960		
Gly Asn Thr Asp Phe Trp Lys Thr Leu Arg Tyr Leu Ser Leu Leu Tyr 965 970 975		
Pro Ala Arg Gly Ser Arg Asn Ile Leu Leu Val Ser Asp Gly His Leu 980 985 990		
Gln Asp Glu Ser Leu Thr Leu Gln Leu Val Lys Arg Ser Arg Pro His 995 1000 1005		
Thr Arg Leu Phe Ala Cys Gly Ile Gly Ser Thr Ala Asn Arg His 1010 1015 1020		
Val Leu Arg Ile Leu Ser Gln Cys Gly Ala Gly Val Phe Glu Tyr 1025 1030 1035		
Phe Asn Ala Lys Ser Lys His Ser Trp Arg Lys Gln Ile Glu Asp 1040 1045 1050		
Gln Met Thr Arg Leu Cys Ser Pro Ser Cys His Ser Val Ser Val 1055 1060 1065		
Lys Trp Gln Gln Leu Asn Pro Asp Ala Pro Glu Ala Leu Gln Ala 1070 1075 1080		
Pro Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu Val 1085 1090 1095		
Tyr Gly Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala Leu 1100 1105 1110		
Ile Gln Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu Leu 1115 1120 1125		
Gln Lys Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg Ala 1130 1135 1140		

Leu Ile	Arg Asp Tyr Glu Asp	Gly Ile Leu His Glu	Asn Glu Thr
1145	1150	1155	
Ser His	Glu Met Lys Lys Gln	Thr Leu Lys Ser Leu	Ile Ile Lys
1160	1165	1170	
Leu Ser	Lys Glu Asn Ser Leu	Ile Thr Gln Phe Thr	Ser Phe Val
1175	1180	1185	
Ala Val	Glu Lys Arg Asp Glu	Asn Glu Ser Pro Phe	Pro Asp Ile
1190	1195	1200	
Pro Lys	Val Ser Glu Leu Ile	Ala Lys Glu Asp Val	Asp Phe Leu
1205	1210	1215	
Pro Tyr	Met Ser Trp Gln Gly	Glu Pro Gln Glu Ala	Val Arg Asn
1220	1225	1230	
Gln Ser	Leu Leu Ala Ser Ser	Glu Trp Pro Glu Leu	Arg Leu Ser
1235	1240	1245	
Lys Arg	Lys His Arg Lys Ile	Pro Phe Ser Lys Arg	Lys Met Glu
1250	1255	1260	
Leu Ser	Gln Pro Glu Val Ser	Glu Asp Phe Glu Glu	Asp Gly Leu
1265	1270	1275	
Gly Val	Leu Pro Ala Phe Thr	Ser Asn Leu Glu Arg	Gly Gly Val
1280	1285	1290	
Glu Lys	Leu Leu Asp Leu Ser	Trp Thr Glu Ser Cys	Lys Pro Thr
1295	1300	1305	
Ala Thr	Glu Pro Leu Phe Lys	Lys Val Ser Pro Trp	Glu Thr Ser
1310	1315	1320	
Thr Ser	Ser Phe Phe Pro Ile	Leu Ala Pro Ala Val	Gly Ser Tyr
1325	1330	1335	
Leu Thr	Pro Thr Thr Arg Ala	His Ser Pro Ala Ser	Leu Ser Phe
1340	1345	1350	
Ala Ser	Tyr Arg Gln Val Ala	Ser Phe Gly Ser Ala	Ala Pro Pro
1355	1360	1365	

Arg	Gln	Phe	Asp	Ala	Ser	Gln	Phe	Ser	Gln	Gly	Pro	Val	Pro	Gly
1370						1375					1380			
Thr	Cys	Ala	Asp	Trp	Ile	Pro	Gln	Ser	Ala	Ser	Cys	Pro	Thr	Gly
1385						1390					1395			
Pro	Pro	Gln	Asn	Pro	Pro	Ser	Ala	Pro	Tyr	Cys	Gly	Ile	Val	Phe
1400						1405					1410			
Ser	Gly	Ser	Ser	Leu	Ser	Ser	Ala	Gln	Ser	Ala	Pro	Leu	Gln	His
1415						1420					1425			
Pro	Gly	Gly	Phe	Thr	Thr	Arg	Pro	Ser	Ala	Gly	Thr	Phe	Pro	Glu
1430						1435					1440			
Leu	Asp	Ser	Pro	Gln	Leu	His	Phe	Ser	Leu	Pro	Thr	Asp	Pro	Asp
1445						1450					1455			
Pro	Ile	Arg	Gly	Phe	Gly	Ser	Tyr	His	Pro	Ser	Ala	Tyr	Ser	Pro
1460						1465					1470			
Phe	His	Phe	Gln	Pro	Ser	Ala	Ala	Ser	Leu	Thr	Ala	Asn	Leu	Arg
1475						1480					1485			
Leu	Pro	Met	Ala	Ser	Ala	Leu	Pro	Glu	Ala	Leu	Cys	Ser	Gln	Ser
1490						1495					1500			
Arg	Thr	Thr	Pro	Val	Asp	Leu	Cys	Leu	Leu	Glu	Glu	Ser	Val	Gly
1505						1510					1515			
Ser	Leu	Glu	Gly	Ser	Arg	Cys	Pro	Val	Phe	Ala	Phe	Gln	Ser	Ser
1520						1525					1530			
Asp	Thr	Glu	Ser	Asp	Glu	Leu	Ser	Glu	Val	Leu	Gln	Asp	Ser	Cys
1535						1540					1545			
Phe	Leu	Gln	Ile	Lys	Cys	Asp	Thr	Lys	Asp	Asp	Ser	Ile	Pro	Cys
1550						1555					1560			
Phe	Leu	Glu	Leu	Lys	Glu	Glu	Asp	Glu	Ile	Val	Cys	Thr	Gln	His
1565						1570					1575			
Trp	Gln	Asp	Ala	Val	Pro	Trp	Thr	Glu	Leu	Leu	Ser	Leu	Gln	Thr

1580	1585	1590
Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu 1595 1600 1605		
Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly 1610 1615 1620		
Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu 1625 1630 1635		
Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu 1640 1645 1650		
Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro 1655 1660 1665		
Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln 1670 1675 1680		
Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile 1685 1690 1695		
Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys 1700 1705 1710		
Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His 1715 1720 1725		
Arg Val Leu His Tyr Ser Gln Gly 1730 1735		

&lt;210&gt; 53

&lt;211&gt; 5211

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Homo sapiens

&lt;400&gt; 53

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<210> 54
<211> 351
<212> PRT
<213> Artificial Sequence

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&lt;220&gt;

<223> *Saccaromyces cerevisiae* and *Homo sapiens*

&lt;400&gt; 54

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu  
 1 5 10 15

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

Gly Ile Pro Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu  
 100 105 110

Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu  
 115 120 125

Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala  
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Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln  
 145 150 155 160

Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile  
 165 170 175

Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln  
 180 185 190

His Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr  
 195 200 205

Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn

210

215

220

Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln  
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Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr  
 245 250 255

Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile  
 260 265 270

Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn  
 275 280 285

Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg  
 290 295 300

Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly  
 305 310 315 320

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 <212> DNA  
 <213> Artificial Sequence

<220>  
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 aaccttaggc tgccaatggc ctctgcttta cctgaggctc tttgcagtca gtcccggact 360  
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aacgactggg actctgccac caagcagttg ctgggactcc agcccataag cactgtgtcc     1020
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&lt;211&gt; 1820

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> *Saccaromyces cerevisiae* and *Homo sapiens*

&lt;400&gt; 56

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35              40              45

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Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
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Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65              70              75              80

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Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85              90              95

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Met Val Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys

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Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser 165 170 175		
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Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu 195 200 205		
Val Lys Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp 210 215 220		
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Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu 275 280 285		
Asp Asp Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser 290 295 300		
Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu Lys Lys 305 310 315 320		
Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu 325 330 335		

Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser  
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Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg  
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Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val  
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Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met  
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Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys  
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Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu  
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Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn  
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Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His  
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Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu  
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Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg  
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Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn  
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Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile  
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Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val  
 545 550 555 560

Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp  
 565 570 575

Ser Leu Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly  
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Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp  
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Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp  
 610 615 620

Ser Val His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu  
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Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr  
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Ile Ile Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro  
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Ser Asp His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe  
 675 680 685

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Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu  
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Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile  
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Val Phe Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys  
 740 745 750

Tyr Ile Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala  
 755 760 765

Phe Ile Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu  
 770 775 780

Ala Gln Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr  
 785 790 795 800

Leu Met Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn



805	810	815
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Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser Leu His		
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Pro Glu Lys Glu Ser Glu Ala Cys Met Leu Val Phe Gln Pro Asp Leu		
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Asp Val Asp Leu Pro Asp Leu Ala Ser Glu Ser Glu Val Ile Ile Cys		
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Leu Asp Cys Ser Ser Ser Met Glu Gly Val Thr Phe Leu Gln Ala Lys		
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Gln Ile Thr Leu His Ala Leu Ser Leu Val Gly Glu Lys Gln Lys Val		
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Gln	Leu	Val	Lys	Arg	Ser	Arg	Pro	His	Thr	Arg	Leu	Phe	Ala	Cys
1085						1090					1095			
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Gln	Cys	Gly	Ala	Gly	Val	Phe	Glu	Tyr	Phe	Asn	Ala	Lys	Ser	Lys
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1160						1165					1170			
Leu	Phe	Arg	Asn	Asp	Arg	Leu	Leu	Val	Tyr	Gly	Phe	Ile	Pro	His
1175						1180					1185			
Cys	Thr	Gln	Ala	Thr	Leu	Cys	Ala	Leu	Ile	Gln	Glu	Lys	Glu	Phe
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His Phe 1535	Ser Leu Pro Thr Asp 1540	Pro Asp Pro Ile Arg Gly Phe Gly 1545
Ser Tyr 1550	His Pro Ser Ala Tyr 1555	Ser Pro Phe His Phe Gln Pro Ser 1560
Ala Ala 1565	Ser Leu Thr Ala Asn 1570	Leu Arg Leu Pro Met Ala Ser Ala 1575
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Leu Cys 1595	Leu Leu Glu Glu Ser 1600	Val Gly Ser Leu Glu Gly Ser Arg 1605
Cys Pro 1610	Val Phe Ala Phe Gln 1615	Ser Ser Asp Thr Glu Ser Asp Glu 1620
Leu Ser 1625	Glu Val Leu Gln Asp 1630	Ser Cys Phe Leu Gln Ile Lys Cys 1635
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Leu Thr 1685	Pro Glu Leu Gly Leu 1690	Ile Leu Asn Leu Asn Thr Asn Gly 1695

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<212> DNA

<213> Artificial Sequence

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<223> *Saccaromyces cerevisiae* and *Homo sapiens*

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<210> 58  
<211> 491  
<212> PRT



&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Homo sapiens

&lt;400&gt; 58

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
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Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
 50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
 115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn  
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly  
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val  
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro  
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser  
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val  
 210 215 220

Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Pro Ala  
 225 230 235 240

Asn Leu Arg Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser  
 245 250 255

Gln Ser Arg Thr Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val  
 260 265 270

Gly Ser Leu Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser  
 275 280 285

Asp Thr Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe  
 290 295 300

Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu  
 305 310 315 320

Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln Asp  
 325 330 335

Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe  
 340 345 350

Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn  
 355 360 365

Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln Ser Leu Gly Val  
 370 375 380

Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala Thr Met Leu Val Leu  
 385 390 395 400

Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu Gly Ile Val Phe Lys Ser  
 405 410 415

Leu Met Lys Met Asp Asp Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala  
 420 425 430

Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp Val Arg Arg Thr Glu Gly  
 435 440 445

Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp  
 450 455 460

Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln Pro Ile Ser Thr Val Ser  
 465 470 475 480

Pro Leu His Arg Val Leu His Tyr Ser Gln Gly  
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<211> 1476

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

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gtcactacct tcacctatgg cgtgcagtgc ttttccagat acccagacca tatgaagcag	240
catgactttt tcaagagcgc catgcccagc ggctatgtgc aggagagaaac catctttttc	300
aaagatgacg ggaactacaa gaccgcgcgt gaagtcaagt tcgaagggtga caccctgggtg	360
aatagaatcg agctgaaggc cattgacttt aaggaggatg gaaacattct cggccacaag	420
ctggaataca actataactc ccacaatgtg tacatcatgg ccgacaagca aaagaatggc	480
atcaagggtc acttcaagat cagacacaaac attgaggatg gatccgtgca gctggccgac	540
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ctgtccaccc agtctgccct gtctaaagat cccaacgaaa agagagacca catggtcctg	660
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<210> 60

<211> 1961

<212> PRT

<213> Artificial Sequence

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<223> synthesized and Homo sapiens

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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu  
20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys  
35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe  
50 55 60

Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln  
65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg  
85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val  
100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile  
115 120 125

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn

130	135	140
Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly		
145	150	155 160
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val		
	165	170 175
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro		
	180	185 190
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser		
	195	200 205
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val		
	210	215 220
Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys Met Val		
	225	230 235 240
Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys Val Lys Tyr Leu		
	245	250 255
Pro Gln Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile Lys Glu Asn Gly		
	260	265 270
Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr His Ile Ile Leu		
	275	280 285
Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn Ser Ile Gln Lys		
	290	295 300
Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp Lys Ser Ile Arg		
	305	310 315 320
Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro Tyr Lys Pro Leu		
	325	330 335
Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser Ser Glu Val Lys		
	340	345 350
Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu Glu Asp Thr Val		
	355	360 365

Glu Leu Thr Glu Phe Gly Met Gln Asn Val Glu Ile Pro His Leu Pro  
 370 375 380

Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu Lys Val Gly Met  
 385 390 395 400

Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln Cys Ser Arg Asp  
 405 410 415

Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe Leu Leu Asp Asp  
 420 425 430

Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys Thr Ser Glu Asp  
 435 440 445

Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu Lys Lys Gln Gly  
 450 455 460

Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr Gln Leu Ala Ser  
 465 470 475 480

Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met Asn Ser Ser Thr  
 485 490 495

Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile Trp Ala Glu Ala  
 500 505 510

Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val Asn Arg Ile Ser  
 515 520 525

Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu Leu Val Lys Ala  
 530 535 540

Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln Lys Met Met Thr  
 545 550 555 560

Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met Pro Lys Glu Val  
 565 570 575

Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys Gln Leu Ile Arg  
 580 585 590

Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys Pro Asn Pro Pro  
 595 600 605

Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile Glu His Val Glu  
610 615 620

Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu Val Leu Gln Asn  
625 630 635 640

His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile Phe Arg Val Gly  
645 650 655

Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu Gly Asn Val Arg  
660 665 670

Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val Gly Ile Leu Cys  
675 680 685

Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg Gly Val Gln Arg  
690 695 700

Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe Ser Asp Ser Leu  
705 710 715 720

Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr Asp Gly Thr Arg  
725 730 735

Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys Met Asp Leu His  
740 745 750

Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly Tyr Asp Ser Val  
755 760 765

His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp Phe Glu Asp Asp  
770 775 780

Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met Lys Tyr Ile Ile  
785 790 795 800

Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe His Pro Ser Asp  
805 810 815

His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser Asn Phe Ser Lys  
820 825 830

Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser Ser Ser Thr Lys

835	840	845
Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro Leu Glu Asp Val		
850	855	860
His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln Val Ile Val Phe		
865	870	875
Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu Ala Lys Tyr Ile		
885	890	895
Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe Glu Ala Phe Ile		
900	905	910
Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys Glu Glu Ala Gln		
915	920	925
Gln Glu Tyr Leu Glu Ala Val Thr Gln Gly His Gly Ala Tyr Leu Met		
930	935	940
Ser Gln Asp Ala Pro Asp Val Phe Thr Val Ser Val Gly Asn Leu Pro		
945	950	955
Pro Lys Ala Lys Val Leu Ile Lys Ile Thr Tyr Ile Thr Glu Leu Ser		
965	970	975
Ile Leu Gly Thr Val Gly Val Phe Phe Met Pro Ala Thr Val Ala Pro		
980	985	990
Trp Gln Gln Asp Lys Ala Leu Asn Glu Asn Leu Gln Asp Thr Val Glu		
995	1000	1005
Lys Ile Cys Ile Lys Glu Ile Gly Thr Lys Gln Ser Phe Ser Leu		
1010	1015	1020
Thr Met Ser Ile Glu Met Pro Tyr Val Ile Glu Phe Ile Phe Ser		
1025	1030	1035
Asp Thr His Glu Leu Lys Gln Lys Arg Thr Asp Cys Lys Ala Val		
1040	1045	1050
Ile Ser Thr Met Glu Gly Ser Ser Leu Asp Ser Ser Gly Phe Ser		
1055	1060	1065



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 Ala Pro Ala Gln Val Pro Ser Leu Phe Arg Asn Asp Arg Leu Leu  
 1310 1315 1320  
  
 Val Tyr Gly Phe Ile Pro His Cys Thr Gln Ala Thr Leu Cys Ala  
 1325 1330 1335  
  
 Leu Ile Gln Glu Lys Glu Phe Cys Thr Met Val Ser Thr Thr Glu  
 1340 1345 1350  
  
 Leu Gln Lys Thr Thr Gly Thr Met Ile His Lys Leu Ala Ala Arg  
 1355 1360 1365  
  
 Ala Leu Ile Arg Asp Tyr Glu Asp Gly Ile Leu His Glu Asn Glu  
 1370 1375 1380  
  
 Thr Ser His Glu Met Lys Lys Gln Thr Leu Lys Ser Leu Ile Ile  
 1385 1390 1395  
  
 Lys Leu Ser Lys Glu Asn Ser Leu Ile Thr Gln Phe Thr Ser Phe  
 1400 1405 1410  
  
 Val Ala Val Glu Lys Arg Asp Glu Asn Glu Ser Pro Phe Pro Asp  
 1415 1420 1425  
  
 Ile Pro Lys Val Ser Glu Leu Ile Ala Lys Glu Asp Val Asp Phe  
 1430 1435 1440  
  
 Leu Pro Tyr Met Ser Trp Gln Gly Glu Pro Gln Glu Ala Val Arg  
 1445 1450 1455  
  
 Asn Gln Ser Leu Leu Ala Ser Ser Glu Trp Pro Glu Leu Arg Leu  
 1460 1465 1470  
  
 Ser Lys Arg Lys His Arg Lys Ile Pro Phe Ser Lys Arg Lys Met  
 1475 1480 1485  
  
 Glu Leu Ser Gln Pro Glu Val Ser Glu Asp Phe Glu Glu Asp Gly  
 1490 1495 1500  
  
 Leu Gly Val Leu Pro Ala Phe Thr Ser Asn Leu Glu Arg Gly Val

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Glu Lys Leu Leu Asp Leu Ser Trp Thr Glu Ser Cys Lys Pro Thr				
1520		1525		1530
Ala Thr Glu Pro Leu Phe Lys Lys Val Ser Pro Trp Glu Thr Ser				
1535		1540		1545
Thr Ser Ser Phe Phe Pro Ile Leu Ala Pro Ala Val Gly Ser Tyr				
1550		1555		1560
Leu Thr Pro Thr Thr Arg Ala His Ser Pro Ala Ser Leu Ser Phe				
1565		1570		1575
Ala Ser Tyr Arg Gln Val Ala Ser Phe Gly Ser Ala Ala Pro Pro				
1580		1585		1590
Arg Gln Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly				
1595		1600		1605
Thr Cys Ala Asp Trp Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly				
1610		1615		1620
Pro Pro Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe				
1625		1630		1635
Ser Gly Ser Ser Leu Ser Ser Ala Gln Ser Ala Pro Leu Gln His				
1640		1645		1650
Pro Gly Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu				
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Leu Asp Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp				
1670		1675		1680
Pro Ile Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro				
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Phe His Phe Gln Pro Ser Ala Ala Ser Leu Thr Ala Asn Leu Arg				
1700		1705		1710
Leu Pro Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser				
1715		1720		1725

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Asp Thr	Glu Ser Asp Glu Leu	Ser Glu Val Leu Gln	Asp Ser Cys
1760		1765	1770
Phe Leu	Gln Ile Lys Cys Asp	Thr Lys Asp Asp Ser	Ile Pro Cys
1775		1780	1785
Phe Leu	Glu Leu Lys Glu Glu	Asp Glu Ile Val Cys	Thr Gln His
1790		1795	1800
Trp Gln	Asp Ala Val Pro Trp	Thr Glu Leu Leu Ser	Leu Gln Thr
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Glu Asp	Gly Phe Trp Lys Leu	Thr Pro Glu Leu Gly	Leu Ile Leu
1820		1825	1830
Asn Leu	Asn Thr Asn Gly Leu	His Ser Phe Leu Lys	Gln Lys Gly
1835		1840	1845
Ile Gln	Ser Leu Gly Val Lys	Gly Arg Glu Cys Leu	Leu Asp Leu
1850		1855	1860
Ile Ala	Thr Met Leu Val Leu	Gln Phe Ile Arg Thr	Arg Leu Glu
1865		1870	1875
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1880		1885	1890
Ser Ile	Ser Arg Asn Ile Pro	Trp Ala Phe Glu Ala	Ile Lys Gln
1895		1900	1905
Ala Ser	Glu Trp Val Arg Arg	Thr Glu Gly Gln Tyr	Pro Ser Ile
1910		1915	1920
Cys Pro	Arg Leu Glu Leu Gly	Asn Asp Trp Asp Ser	Ala Thr Lys
1925		1930	1935
Gln Leu	Leu Gly Leu Gln Pro	Ile Ser Thr Val Ser	Pro Leu His
1940		1945	1950

Arg Val Leu His Tyr Ser Gln Gly  
1955 1960

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<220>  
<223> synthesized and Homo sapiens

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aagaaagtca gtccatggga aacatctact tctagctttt ttctattttt ggctccggcc	4680
gttggttctt atcttcccc gactaccgcg gctcacagtc ctgcttctt gtcttttgcc	4740
tcatatcgtc aggtagctag ttctggttca gctgctctc ccagacagtt tgatgcatct	4800

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&lt;210&gt; 62

&lt;211&gt; 385

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Levivirus and Homo sapiens

&lt;400&gt; 62

```

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10           15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20           25           30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

```



35

40

45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
 115 120 125

Ile Tyr Gly Ile Pro Ala Asn Leu Arg Leu Pro Met Ala Ser Ala Leu  
 130 135 140

Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro Val Asp Leu Cys  
 145 150 155 160

Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser Arg Cys Pro Val  
 165 170 175

Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu Leu Ser Glu Val  
 180 185 190

Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp Thr Lys Asp Asp  
 195 200 205

Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp Glu Ile Val Cys  
 210 215 220

Thr Gln His Trp Gln Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu  
 225 230 235 240

Gln Thr Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile  
 245 250 255

Leu Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly  
 260 265 270

Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile  
 275 280 285

Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu  
 290 295 300

Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile Ser  
 305 310 315 320

Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser Glu Trp  
 325 330 335

Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro Arg Leu Glu  
 340 345 350

Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu Leu Gly Leu Gln  
 355 360 365

Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu His Tyr Ser Gln  
 370 375 380

Gly  
 385

<210> 63  
 <211> 1158  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Homo sapiens

<400> 63  
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 caggcttaca aagtaacctg tagcggttcgt cagagctctg cgcagaatcg caaatacacc 180  
 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gcttctgtga 240  
 gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300  
 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360  
 tcagcaatcg cagcaaactc cggcatctac ggaattcctg ccaaccttag gctgccaatg 420  
 gcctctgctt tacctgaggc tctttgcagt cagtcccga ctacccaggt agatctctgt 480  
 cttctagaag aatcagtagg cagtctcgaa ggaagtcgat gtctgtctt tgcttttcaa 540

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agttctgaca cagaaagtga tgagctatca gaagtacttc aagacagctg cttttttacaa      600
ataaagtgtg atacaaaaga tgacagtatc ccgtgctttc tggaattaaa agaagaggat      660
gaaatagtgt gcacacaaca ctggcaggat gctgtgcctt ggacagaact cctcagtcta      720
cagacagagg atggcttctg gaaacttaca ccagaactgg gacttatatt aaatcttaat      780
acaaatgggt tgcacagctt tcttaaacia aaaggcattc aatctctagg tgtaaaagga      840
agagaatgtc tcctggacct aattgccaca atgctggtac tacagtttat tcgcaccagg      900
ttggaaaaag agggaaatagt gttcaaata ctgatgaaaa tggatgaccc ttctatttcc      960
aggaatattc cctgggcttt tgaggcaata aagcaagcaa gtgaatgggt aagaagaact     1020
gaaggacagt acccatctat ctgcccacgg cttgaactgg ggaacgactg ggactctgcc     1080
accaagcagt tgctgggact ccagcccata agcactgtgt cccctcttca tagagtcctc     1140
cattacagtc aaggctaa                                     1158

```

&lt;210&gt; 64

&lt;211&gt; 1854

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Levivirus and Homo sapiens

&lt;400&gt; 64

```

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1              5              10              15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
                20              25              30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
        35              40              45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
        50              55              60

```

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
        65              70              75              80

```

```

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
        85              90              95

```

```

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu

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100	105	110
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly		
115	120	125
Ile Tyr Met Val Met Gly Ile Phe Ala Asn Cys Ile Phe Cys Leu Lys		
130	135	140
Val Lys Tyr Leu Pro Gln Gln Gln Lys Lys Lys Leu Gln Thr Asp Ile		
145	150	155
Lys Glu Asn Gly Gly Lys Phe Ser Phe Ser Leu Asn Pro Gln Cys Thr		
165	170	175
His Ile Ile Leu Asp Asn Ala Asp Val Leu Ser Gln Tyr Gln Leu Asn		
180	185	190
Ser Ile Gln Lys Asn His Val His Ile Ala Asn Pro Asp Phe Ile Trp		
195	200	205
Lys Ser Ile Arg Glu Lys Arg Leu Leu Asp Val Lys Asn Tyr Asp Pro		
210	215	220
Tyr Lys Pro Leu Asp Ile Thr Pro Pro Pro Asp Gln Lys Ala Ser Ser		
225	230	235
Ser Glu Val Lys Thr Glu Gly Leu Cys Pro Asp Ser Ala Thr Glu Glu		
245	250	255
Glu Asp Thr Val Glu Leu Thr Glu Phe Gly Met Gln Asn Val Glu Ile		
260	265	270
Pro His Leu Pro Gln Asp Phe Glu Val Ala Lys Tyr Asn Thr Leu Glu		
275	280	285
Lys Val Gly Met Glu Gly Gly Gln Glu Ala Val Val Val Glu Leu Gln		
290	295	300
Cys Ser Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile Ser Ser His Phe		
305	310	315
Leu Leu Asp Asp Gly Met Glu Thr Arg Arg Gln Phe Ala Ile Lys Lys		
325	330	335

Thr Ser Glu Asp Ala Ser Glu Tyr Phe Glu Asn Tyr Ile Glu Glu Leu  
 340 345 350

Lys Lys Gln Gly Phe Leu Leu Arg Glu His Phe Thr Pro Glu Ala Thr  
 355 360 365

Gln Leu Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu Glu Glu Val Met  
 370 375 380

Asn Ser Ser Thr Leu Ser Gln Glu Val Ser Asp Leu Val Glu Met Ile  
 385 390 395 400

Trp Ala Glu Ala Leu Gly His Leu Glu His Met Leu Leu Lys Pro Val  
 405 410 415

Asn Arg Ile Ser Leu Asn Asp Val Ser Lys Ala Glu Gly Ile Leu Leu  
 420 425 430

Leu Val Lys Ala Ala Leu Lys Asn Gly Glu Thr Ala Glu Gln Leu Gln  
 435 440 445

Lys Met Met Thr Glu Phe Tyr Arg Leu Ile Pro His Lys Gly Thr Met  
 450 455 460

Pro Lys Glu Val Asn Leu Gly Leu Leu Ala Lys Lys Ala Asp Leu Cys  
 465 470 475 480

Gln Leu Ile Arg Asp Met Val Asn Val Cys Glu Thr Asn Leu Ser Lys  
 485 490 495

Pro Asn Pro Pro Ser Leu Ala Lys Tyr Arg Ala Leu Arg Cys Lys Ile  
 500 505 510

Glu His Val Glu Gln Asn Thr Glu Glu Phe Leu Arg Val Arg Lys Glu  
 515 520 525

Val Leu Gln Asn His His Ser Lys Ser Pro Val Asp Val Leu Gln Ile  
 530 535 540

Phe Arg Val Gly Arg Val Asn Glu Thr Thr Glu Phe Leu Ser Lys Leu  
 545 550 555 560

Gly Asn Val Arg Pro Leu Leu His Gly Ser Pro Val Gln Asn Ile Val  
 565 570 575

Gly Ile Leu Cys Arg Gly Leu Leu Leu Pro Lys Val Val Glu Asp Arg  
 580 585 590

Gly Val Gln Arg Thr Asp Val Gly Asn Leu Gly Ser Gly Ile Tyr Phe  
 595 600 605

Ser Asp Ser Leu Ser Thr Ser Ile Lys Tyr Ser His Pro Gly Glu Thr  
 610 615 620

Asp Gly Thr Arg Leu Leu Leu Ile Cys Asp Val Ala Leu Gly Lys Cys  
 625 630 635 640

Met Asp Leu His Glu Lys Asp Phe Pro Leu Thr Glu Ala Pro Pro Gly  
 645 650 655

Tyr Asp Ser Val His Gly Val Ser Gln Thr Ala Ser Val Thr Thr Asp  
 660 665 670

Phe Glu Asp Asp Glu Phe Val Val Tyr Lys Thr Asn Gln Val Lys Met  
 675 680 685

Lys Tyr Ile Ile Lys Phe Ser Met Pro Gly Asp Gln Ile Lys Asp Phe  
 690 695 700

His Pro Ser Asp His Thr Glu Leu Glu Glu Tyr Arg Pro Glu Phe Ser  
 705 710 715 720

Asn Phe Ser Lys Val Glu Asp Tyr Gln Leu Pro Asp Ala Lys Thr Ser  
 725 730 735

Ser Ser Thr Lys Ala Gly Leu Gln Asp Ala Ser Gly Asn Leu Val Pro  
 740 745 750

Leu Glu Asp Val His Ile Lys Gly Arg Ile Ile Asp Thr Val Ala Gln  
 755 760 765

Val Ile Val Phe Gln Thr Tyr Thr Asn Lys Ser His Val Pro Ile Glu  
 770 775 780

Ala Lys Tyr Ile Phe Pro Leu Asp Asp Lys Ala Ala Val Cys Gly Phe  
 785 790 795 800

Glu Ala Phe Ile Asn Gly Lys His Ile Val Gly Glu Ile Lys Glu Lys

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Lys	Gln	Lys	Val	Asn	Ile	Ile	Gln	Phe	Gly	Thr	Gly	Tyr	Lys	Glu
1040						1045					1050			
Leu	Phe	Ser	Tyr	Pro	Lys	His	Ile	Thr	Ser	Asn	Thr	Thr	Ala	Ala
1055						1060					1065			
Glu	Phe	Ile	Met	Ser	Ala	Thr	Pro	Thr	Met	Gly	Asn	Thr	Asp	Phe
1070						1075					1080			
Trp	Lys	Thr	Leu	Arg	Tyr	Leu	Ser	Leu	Leu	Tyr	Pro	Ala	Arg	Gly
1085						1090					1095			
Ser	Arg	Asn	Ile	Leu	Leu	Val	Ser	Asp	Gly	His	Leu	Gln	Asp	Glu
1100						1105					1110			
Ser	Leu	Thr	Leu	Gln	Leu	Val	Lys	Arg	Ser	Arg	Pro	His	Thr	Arg
1115						1120					1125			
Leu	Phe	Ala	Cys	Gly	Ile	Gly	Ser	Thr	Ala	Asn	Arg	His	Val	Leu
1130						1135					1140			
Arg	Ile	Leu	Ser	Gln	Cys	Gly	Ala	Gly	Val	Phe	Glu	Tyr	Phe	Asn
1145						1150					1155			
Ala	Lys	Ser	Lys	His	Ser	Trp	Arg	Lys	Gln	Ile	Glu	Asp	Gln	Met
1160						1165					1170			
Thr	Arg	Leu	Cys	Ser	Pro	Ser	Cys	His	Ser	Val	Ser	Val	Lys	Trp
1175						1180					1185			
Gln	Gln	Leu	Asn	Pro	Asp	Ala	Pro	Glu	Ala	Leu	Gln	Ala	Pro	Ala
1190						1195					1200			
Gln	Val	Pro	Ser	Leu	Phe	Arg	Asn	Asp	Arg	Leu	Leu	Val	Tyr	Gly
1205						1210					1215			
Phe	Ile	Pro	His	Cys	Thr	Gln	Ala	Thr	Leu	Cys	Ala	Leu	Ile	Gln
1220						1225					1230			
Glu	Lys	Glu	Phe	Cys	Thr	Met	Val	Ser	Thr	Thr	Glu	Leu	Gln	Lys
1235						1240					1245			
Thr	Thr	Gly	Thr	Met	Ile	His	Lys	Leu	Ala	Ala	Arg	Ala	Leu	Ile
1250						1255					1260			



Arg Asp	Tyr Glu Asp Gly Ile	Leu His Glu Asn Glu	Thr Ser His
1265	1270	1275	
Glu Met	Lys Lys Gln Thr Leu	Lys Ser Leu Ile Ile	Lys Leu Ser
1280	1285	1290	
Lys Glu	Asn Ser Leu Ile Thr	Gln Phe Thr Ser Phe	Val Ala Val
1295	1300	1305	
Glu Lys	Arg Asp Glu Asn Glu	Ser Pro Phe Pro Asp	Ile Pro Lys
1310	1315	1320	
Val Ser	Glu Leu Ile Ala Lys	Glu Asp Val Asp Phe	Leu Pro Tyr
1325	1330	1335	
Met Ser	Trp Gln Gly Glu Pro	Gln Glu Ala Val Arg	Asn Gln Ser
1340	1345	1350	
Leu Leu	Ala Ser Ser Glu Trp	Pro Glu Leu Arg Leu	Ser Lys Arg
1355	1360	1365	
Lys His	Arg Lys Ile Pro Phe	Ser Lys Arg Lys Met	Glu Leu Ser
1370	1375	1380	
Gln Pro	Glu Val Ser Glu Asp	Phe Glu Glu Asp Gly	Leu Gly Val
1385	1390	1395	
Leu Pro	Ala Phe Thr Ser Asn	Leu Glu Arg Gly Gly	Val Glu Lys
1400	1405	1410	
Leu Leu	Asp Leu Ser Trp Thr	Glu Ser Cys Lys Pro	Thr Ala Thr
1415	1420	1425	
Glu Pro	Leu Phe Lys Lys Val	Ser Pro Trp Glu Thr	Ser Thr Ser
1430	1435	1440	
Ser Phe	Phe Pro Ile Leu Ala	Pro Ala Val Gly Ser	Tyr Leu Thr
1445	1450	1455	
Pro Thr	Thr Arg Ala His Ser	Pro Ala Ser Leu Ser	Phe Ala Ser
1460	1465	1470	
Tyr Arg	Gln Val Ala Ser Phe	Gly Ser Ala Ala Pro	Pro Arg Gln

1475		1480		1485
Phe Asp Ala Ser Gln Phe Ser Gln Gly Pro Val Pro Gly Thr Cys				
1490		1495		1500
Ala Asp Trp Ile Pro Gln Ser Ala Ser Cys Pro Thr Gly Pro Pro				
1505		1510		1515
Gln Asn Pro Pro Ser Ala Pro Tyr Cys Gly Ile Val Phe Ser Gly				
1520		1525		1530
Ser Ser Leu Ser Ser Ala Gln Ser Ala Pro Leu Gln His Pro Gly				
1535		1540		1545
Gly Phe Thr Thr Arg Pro Ser Ala Gly Thr Phe Pro Glu Leu Asp				
1550		1555		1560
Ser Pro Gln Leu His Phe Ser Leu Pro Thr Asp Pro Asp Pro Ile				
1565		1570		1575
Arg Gly Phe Gly Ser Tyr His Pro Ser Ala Tyr Ser Pro Phe His				
1580		1585		1590
Phe Gln Pro Ser Ala Ala Ser Leu Thr Ala Asn Leu Arg Leu Pro				
1595		1600		1605
Met Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr				
1610		1615		1620
Thr Pro Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu				
1625		1630		1635
Glu Gly Ser Arg Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr				
1640		1645		1650
Glu Ser Asp Glu Leu Ser Glu Val Leu Gln Asp Ser Cys Phe Leu				
1655		1660		1665
Gln Ile Lys Cys Asp Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu				
1670		1675		1680
Glu Leu Lys Glu Glu Asp Glu Ile Val Cys Thr Gln His Trp Gln				
1685		1690		1695

Asp Ala Val Pro Trp Thr Glu Leu Leu Ser Leu Gln Thr Glu Asp  
1700 1705 1710

Gly Phe Trp Lys Leu Thr Pro Glu Leu Gly Leu Ile Leu Asn Leu  
1715 1720 1725

Asn Thr Asn Gly Leu His Ser Phe Leu Lys Gln Lys Gly Ile Gln  
1730 1735 1740

Ser Leu Gly Val Lys Gly Arg Glu Cys Leu Leu Asp Leu Ile Ala  
1745 1750 1755

Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg Leu Glu Lys Glu  
1760 1765 1770

Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp Pro Ser Ile  
1775 1780 1785

Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln Ala Ser  
1790 1795 1800

Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys Pro  
1805 1810 1815

Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu  
1820 1825 1830

Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His Arg Val  
1835 1840 1845

Leu His Tyr Ser Gln Gly  
1850

<210> 65  
<211> 5565  
<212> DNA  
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<223> Levivirus and Homo sapiens

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caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc 180

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gaatttctca gggttagaaa agaggttttg cagaatcctc acagtaagag cccagtggat 1620  
gtcttgcaga tatttagagt tggcagagt aatgaaacca cagagttttt gagcaaactt 1680  
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<210> 66  
<211> 550  
<212> PRT  
<213> *Photinus pyralis*

<400> 66

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20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu  
85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg  
100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val  
115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro  
130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  
145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe  
165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile  
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val  
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp  
 210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val  
 225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu  
 245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu  
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val  
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr  
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser  
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile  
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr  
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe  
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly  
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly  
 405 410 415



Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe  
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln  
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile  
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu  
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys  
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu  
 500 505 510

Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly  
 515 520 525

Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys  
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Gly Gly Lys Ile Ala Val  
 545 550

<210> 67  
 <211> 1654  
 <212> DNA  
 <213> *Photinus pyralis*

<400> 67  
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 gcttttacag atgcacatat cgaggtggac atcacttacg ctgagtactt cgaaatgtcc 180  
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 aaaaagctcc caatcatcca aaaaattatt atcatggatt ctaaaacgga ttaccaggga 480

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<210> 68  
 <211> 805  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> *Photinus pyralis* and *Homo sapiens*

<400> 68

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Leu	Glu	Asp	Gly	Thr	Ala	Gly	Glu	Gln	Leu	His	Lys	Ala	Met	Lys	Arg
			20					25					30		

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
 50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
 65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu  
 85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg  
 100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val  
 115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro  
 130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  
 145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe  
 165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile  
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val  
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp  
 210 215 220

Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val  
 225 230 235 240

Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu  
 245 250 255

Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu  
 260 265 270

Phe Leu Arg Ser Leu Gln Asp Tyr Lys Ile Gln Ser Ala Leu Leu Val  
 275 280 285

Pro Thr Leu Phe Ser Phe Phe Ala Lys Ser Thr Leu Ile Asp Lys Tyr  
 290 295 300

Asp Leu Ser Asn Leu His Glu Ile Ala Ser Gly Gly Ala Pro Leu Ser  
 305 310 315 320

Lys Glu Val Gly Glu Ala Val Ala Lys Arg Phe His Leu Pro Gly Ile  
 325 330 335

Arg Gln Gly Tyr Gly Leu Thr Glu Thr Thr Ser Ala Ile Leu Ile Thr  
 340 345 350

Pro Glu Gly Asp Asp Lys Pro Gly Ala Val Gly Lys Val Val Pro Phe  
 355 360 365

Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val  
 370 375 380

Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly  
 385 390 395 400

Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly  
 405 410 415

Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe  
 420 425 430

Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln  
 435 440 445

Val Ala Pro Ala Glu Leu Glu Ser Ile Leu Leu Gln His Pro Asn Ile  
 450 455 460

Phe Asp Ala Gly Val Ala Gly Leu Pro Asp Asp Asp Ala Gly Glu Leu  
 465 470 475 480

Pro Ala Ala Val Val Val Leu Glu His Gly Lys Thr Met Thr Glu Lys  
 485 490 495

Glu Ile Val Asp Tyr Val Ala Ser Gln Val Thr Thr Ala Lys Lys Leu

500	505	510
Arg Gly Gly Val Val Phe Val Asp Glu Val Pro Lys Gly Leu Thr Gly		
515	520	525
Lys Leu Asp Ala Arg Lys Ile Arg Glu Ile Leu Ile Lys Ala Lys Lys		
530	535	540
Gly Gly Lys Ile Ala Val Gly Ile Pro Ala Asn Leu Arg Leu Pro Met		
545	550	555
Ala Ser Ala Leu Pro Glu Ala Leu Cys Ser Gln Ser Arg Thr Thr Pro		
565	570	575
Val Asp Leu Cys Leu Leu Glu Glu Ser Val Gly Ser Leu Glu Gly Ser		
580	585	590
Arg Cys Pro Val Phe Ala Phe Gln Ser Ser Asp Thr Glu Ser Asp Glu		
595	600	605
Leu Ser Glu Val Leu Gln Asp Ser Cys Phe Leu Gln Ile Lys Cys Asp		
610	615	620
Thr Lys Asp Asp Ser Ile Pro Cys Phe Leu Glu Leu Lys Glu Glu Asp		
625	630	635
Glu Ile Val Cys Thr Gln His Trp Gln Asp Ala Val Pro Trp Thr Glu		
645	650	655
Leu Leu Ser Leu Gln Thr Glu Asp Gly Phe Trp Lys Leu Thr Pro Glu		
660	665	670
Leu Gly Leu Ile Leu Asn Leu Asn Thr Asn Gly Leu His Ser Phe Leu		
675	680	685
Lys Gln Lys Gly Ile Gln Ser Leu Gly Val Lys Gly Arg Glu Cys Leu		
690	695	700
Leu Asp Leu Ile Ala Thr Met Leu Val Leu Gln Phe Ile Arg Thr Arg		
705	710	715
Leu Glu Lys Glu Gly Ile Val Phe Lys Ser Leu Met Lys Met Asp Asp		
725	730	735

Pro Ser Ile Ser Arg Asn Ile Pro Trp Ala Phe Glu Ala Ile Lys Gln  
 740 745 750

Ala Ser Glu Trp Val Arg Arg Thr Glu Gly Gln Tyr Pro Ser Ile Cys  
 755 760 765

Pro Arg Leu Glu Leu Gly Asn Asp Trp Asp Ser Ala Thr Lys Gln Leu  
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Leu Gly Leu Gln Pro Ile Ser Thr Val Ser Pro Leu His Arg Val Leu  
 785 790 795 800

His Tyr Ser Gln Gly  
 805

<210> 69  
 <211> 2418  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Photinus pyralis and Homo sapiens

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&lt;210&gt; 70

&lt;211&gt; 2274

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Photinus pyralis and Homo sapiens

&lt;400&gt; 70

Met Glu Asp Ala Lys Asn Ile Lys Lys Gly Pro Ala Pro Phe Tyr Pro  
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Leu Glu Asp Gly Thr Ala Gly Glu Gln Leu His Lys Ala Met Lys Arg  
 20 25 30

Tyr Ala Leu Val Pro Gly Thr Ile Ala Phe Thr Asp Ala His Ile Glu  
 35 40 45

Val Asp Ile Thr Tyr Ala Glu Tyr Phe Glu Met Ser Val Arg Leu Ala  
 50 55 60

Glu Ala Met Lys Arg Tyr Gly Leu Asn Thr Asn His Arg Ile Val Val  
 65 70 75 80

Cys Ser Glu Asn Ser Leu Gln Phe Phe Met Pro Val Leu Gly Ala Leu  
 85 90 95

Phe Ile Gly Val Ala Val Ala Pro Ala Asn Asp Ile Tyr Asn Glu Arg  
 100 105 110

Glu Leu Leu Asn Ser Met Gly Ile Ser Gln Pro Thr Val Val Phe Val  
 115 120 125

Ser Lys Lys Gly Leu Gln Lys Ile Leu Asn Val Gln Lys Lys Leu Pro  
 130 135 140

Ile Ile Gln Lys Ile Ile Ile Met Asp Ser Lys Thr Asp Tyr Gln Gly  
 145 150 155 160

Phe Gln Ser Met Tyr Thr Phe Val Thr Ser His Leu Pro Pro Gly Phe  
 165 170 175

Asn Glu Tyr Asp Phe Val Pro Glu Ser Phe Asp Arg Asp Lys Thr Ile  
 180 185 190

Ala Leu Ile Met Asn Ser Ser Gly Ser Thr Gly Leu Pro Lys Gly Val  
 195 200 205

Ala Leu Pro His Arg Thr Ala Cys Val Arg Phe Ser His Ala Arg Asp



210	215	220
Pro Ile Phe Gly Asn Gln Ile Ile Pro Asp Thr Ala Ile Leu Ser Val		
225	230	235 240
Val Pro Phe His His Gly Phe Gly Met Phe Thr Thr Leu Gly Tyr Leu		
	245	250 255
Ile Cys Gly Phe Arg Val Val Leu Met Tyr Arg Phe Glu Glu Glu Leu		
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Phe Glu Ala Lys Val Val Asp Leu Asp Thr Gly Lys Thr Leu Gly Val		
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Asn Gln Arg Gly Glu Leu Cys Val Arg Gly Pro Met Ile Met Ser Gly		
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Tyr Val Asn Asn Pro Glu Ala Thr Asn Ala Leu Ile Asp Lys Asp Gly		
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Trp Leu His Ser Gly Asp Ile Ala Tyr Trp Asp Glu Asp Glu His Phe		
	420	425 430
Phe Ile Val Asp Arg Leu Lys Ser Leu Ile Lys Tyr Lys Gly Tyr Gln		
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Pro Gln Cys Thr His Ile Ile Leu Asp Asn Ala Asp Val Leu Ser Gln  
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Tyr Gln Leu Asn Ser Ile Gln Lys Asn His Val His Ile Ala Asn Pro  
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Asn Thr Leu Glu Lys Val Gly Met Glu Gly Gly Gln Glu Ala Val Val  
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Val Glu Leu Gln Cys Ser Arg Asp Ser Arg Asp Cys Pro Phe Leu Ile  
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Ser Ser His Phe Leu Leu Asp Asp Gly Met Glu Thr Arg Arg Gln Phe  
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Pro Glu Ala Thr Gln Leu Ala Ser Glu Gln Leu Gln Ala Leu Leu Leu  
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gtgccttgga cagaactcct cagtctacag acagaggatg gcttctggaa acttacacca 6420
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ctggtactac agttttattcg caccagggtg gaaaaagagg gaatagtgtt caaatcactg 6600
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caagcaagtg aatgggtaag aagaactgaa ggacagtacc catctatctg cccacggctt 6720
gaactgggga acgactggga ctctgccacc aagcagttgc tgggactcca gcccataagc 6780
actgtgtccc ctcttcatag agtcctccat tacagtcaag gctaa 6825

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<210> 72  
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 <212> PRT  
 <213> *Drosophila melanogaster*

<400> 72

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Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys
1           5           10          15

```

<210> 73  
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 <212> DNA  
 <213> *Drosophila melanogaster*

<400> 73  
 cgacagatca agatctgggt tcagaacgca cggatgaagt ggaagaagtg a 51

<210> 74  
 <211> 909  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> *Homo sapiens* and *Drosophila melanogaster*

<400> 74

```

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10          15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
35           40           45

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln  
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr



515					520					525					
Ile	Glu	Thr	Ala	Asp	His	Ala	Arg	Leu	Gln	Leu	Gln	Leu	Ala	Tyr	Asn
530						535					540				
Trp	His	Phe	Glu	Val	Asn	Asp	Arg	Lys	Asp	Pro	Gln	Glu	Thr	Ala	Lys
545					550					555					560
Leu	Phe	Ser	Val	Pro	Asp	Phe	Val	Gly	Asp	Ala	Cys	Lys	Ala	Ile	Ala
				565					570					575	
Ser	Arg	Val	Arg	Gly	Ala	Val	Ala	Ser	Val	Thr	Phe	Asp	Asp	Phe	His
			580					585					590		
Lys	Asn	Ser	Ala	Arg	Ile	Ile	Arg	Thr	Ala	Val	Phe	Gly	Phe	Glu	Thr
			595				600					605			
Ser	Glu	Ala	Lys	Gly	Pro	Asp	Gly	Met	Ala	Leu	Pro	Arg	Pro	Arg	Asp
	610					615					620				
Gln	Ala	Val	Phe	Pro	Gln	Asn	Gly	Leu	Val	Val	Ser	Ser	Val	Asp	Val
625					630					635					640
Gln	Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala	Leu	Gln	Arg
				645					650					655	
Ser	Val	Gln	Leu	Ala	Ile	Glu	Ile	Thr	Thr	Asn	Ser	Gln	Glu	Ala	Ala
			660					665					670		
Ala	Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg	Gly	Arg	Leu
		675					680					685			
Glu	Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys	Ala	Arg	Lys
	690					695					700				
Glu	Leu	Leu	Glu	Leu	Glu	Ala	Leu	Ser	Met	Ala	Val	Glu	Ser	Thr	Gly
705					710					715					720
Thr	Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala	Arg	Ile	Glu
				725					730					735	
Gly	Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln	Ala	Leu	Ala
			740					745					750		

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
 755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
 785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Arg Gln Ile  
 885 890 895

Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys  
 900 905

<210> 75  
 <211> 2730  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens and Drosophila melanogaster

<400> 75  
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 gagagggtac tgtttgcccc catgcgcac gtgaccgtcc cccacgtca ctactgcaca 180  
 gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgtttgatgt cacagggcaa 240  
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ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caaactgcc	360
ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga	420
gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg	480
gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgaag	540
gagtgctggg accgggacgg caaggagagg gtgacagggg aagaatggct ggtcaccaca	600
gtaggggcgt acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc	660
cttacggaaa agacagccct gcacctcgg gctcggcgga acttcggga cttcagggga	720
gtgtcccgcc gcaactgggga ggagtggctg gtaacagtgc aggacacaga ggcccacgtg	780
ccagatgtcc acgaggaggt gctgggggtt gtgccatca ccacctggg cccccacaac	840
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gtggtcaagg gagagaagtc ttttttcctc cagccaggag agcagctgga acaaggcatc	960
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ctcttttcag tgccagactt tgtaggtgat gcctgcaaag ccatcgcac cggggtgcgg	1740
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```

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cagaacgcac ggatgaagtg gaagaagtga 2730

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&lt;210&gt; 76

&lt;211&gt; 877

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rattus norvegicus and Drosophila melanogaster

&lt;400&gt; 76

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
          20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
          35           40           45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
          50           55           60

```

```

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
65           70           75           80

```

```

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
          85           90           95

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys  
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala

[illegible]

252/429



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 aaagcccgca aggaactctt ggagcttgag gctatgagca tggctgtgga gagcacgggt 2160  
 aatgccaaag cagaggctga gtcccgtgca gaggcagcga ggatcgaagg agaaggctct 2220  
 gtgctgcagg ccaagctcaa ggcacaggcg ctagccattg agacggaggc tgagttggag 2280  
 cgagtaaaga aagtacgaga gatggaactg atctatgcc gggcccagtt ggagctggag 2340  
 gtgagcaagg cgcagcagct tgccaatgtg gagggcaaaga agttcaagga gatgacagag 2400  
 gcactgggac ccggcaccat caggacactg gctgtggccg ggccagagat gcaggtgaaa 2460  
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 <212> PRT  
 <213> Human immunodeficiency virus type 1

<400> 78

Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
 1 5 10

<210> 79  
 <211> 33  
 <212> DNA  
 <213> Human immunodeficiency virus type 1

<400> 79

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33

<210> 80  
 <211> 904  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Homo sapiens and Human immunodeficiency virus type 1

<400> 80

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
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His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln  
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 530 535 540

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys  
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His

580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr 595 600 605		
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp 610 615 620		
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625 630 635 640		
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645 650 655		
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660 665 670		
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675 680 685		
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690 695 700		
Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly 705 710 715 720		
Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu 725 730 735		
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala 740 745 750		
Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu 755 760 765		
Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala 770 775 780		
Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu 785 790 795 800		
Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu 805 810 815		

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
                   820                                  825                                  830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
                   835                                  840                                  845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
                   850                                  855                                  860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
                   865                                  870                                  875                                  880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly Arg  
                                   885                                  890                                  895

Lys Lys Arg Arg Gln Arg Arg Arg  
                                   900

<210> 81  
 <211> 2715  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Homo sapiens and Human immunodeficiency virus type 1

<400> 81  
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 gagagggtag tgtttgcccc catgcgcacg gtgaccgtcc cccacagtca ctactgcaca 180  
 gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgtttgatgt cacagggcaa 240  
 gttcggcttc gccacgtga cctcgagatc cggctggccc aggaccctt cccctgtac 300  
 ccaggggagg tgctggaaaa ggacatcaca ccctgcagg tggttctgcc caactgcc 360  
 ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga 420  
 gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg 480  
 gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgcaag 540  
 gagtgtctgg accgggacgg caaggagagg gtgacagggg aagaatggct ggtcaccaca 600  
 gtaggggctg acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc 660  
 cttacggaaa agacagccct gcacctccg gctcggcgga acttccggga cttcagggga 720  
 gtgtcccgcc gcactgggga ggagtggctg gtaacagtgc aggacacaga ggcccacgtg 780

ccagatgtcc acgaggaggt gctggggggt gtgcccata ccaccctggg cccccacaac	840
tactgctga ttctcgaccc tgtcggaccg gatggcaaga atcagctggg gcagaagcgc	900
gtggtcaagg gagagaagtc ttttttcctc cagccaggag agcagctgga acaaggcatc	960
caggatgtgt atgtgctgtc ggagcagcag gggctgctgc tgagggccct gcagcccctg	1020
gaggaggggg aggatgagga gaaggtctca caccaggctg gggaccactg gctcatccgc	1080
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cctctagacg agaacgaggg catctatgtg caggatgtca agaccggaaa ggtgcgcgct	1200
gtgattggaa gcacctacat gctgaccag gacgaagtcc tgtgggagaa agagctgcct	1260
cccgggggtg aggagctgct gaacaagggg caggaccctc tggcagacag gggtgagaag	1320
gacacagcta agagcctcca gcccttggcg ccccggaaca agaccctgtg ggtcagctac	1380
cgctgcccc acaacgctgc ggtgcagggt tacgactacc gagagaagcg agcccgctg	1440
gtcttcgggc ctgagctggt gtcgctgggt cctgaggagc agttcacagt gttgtccctc	1500
tcagctgggc ggcccaagcg tccccatgcc cgccgtgcgc tctgctgct gctggggcct	1560
gacttcttca cagacgtcat caccatcgaa acggcggatc atgccaggct gcaactgcag	1620
ctggcctaca actggcactt tgaggtgaat gaccggaagg accccaaga gacggccaag	1680
ctcttttcag tgccagactt ttaggtgat gcctgcaaag ccatcgcatc ccgggtgcgg	1740
ggggccgtgg cctctgtcac ttctgatgac ttccataaga actcagcccc catcattcgc	1800
actgctgtct ttggctttga gacctcgaa gcgaagggcc ccgatggcat ggccctgccc	1860
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cagtcagtgg agcctgtgga tcagaggacc cgggacgccc tgcaacgcag cgtccagctg	1980
gccatcgaga tcaccaccaa ctcccaggaa gcggcggcca agcatgaggc tcagagactg	2040
gagcaggaag ccgcggccg gcttgagcgg cagaagatcc tggaccagtc agaagccgag	2100
aaagctcgca aggaactttt ggagctggag gctctgagca tggccgtgga gagcaccggg	2160
actgccaagg cggaggccga gtcccgtgcg gaggcagccc ggattgaggg agaagggctc	2220
gtgctgcagg ccaagctaaa agcacaggcc ttggccattg aaacggaggc tgagctccag	2280
agggccaga aggtccgaga gctggaactg gtctatgccc gggcccagct ggagctggag	2340
gtgagcaagg ctcagcagct ggctgaggtg gaggtgaaga agttcaagca gatgacagag	2400
gccataggcc ccagcaccat caggacctt gctgtggctg ggcctgagat gcaggtaaaa	2460
ctgctccagt ccctgggcct gaaatcaacc ctcatcacc atggctccac tcccatcaac	2520

```

ctctttcaaca cagccttttg gctgctgggg atggggcccg agggtcagcc cctgggcaga    2580
aggggtggcca gtgggcccag ccctggggag gggatatccc ccagttctgc tcaggcccct    2640
caagctcctg gagacaacca cgtgggtgcct gtactgcgct acgggcggaa gaagcggcga    2700
cagaggcgac ggtga                                                    2715

```

&lt;210&gt; 82

&lt;211&gt; 872

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rattus norvegicus and Human immunodeficiency virus type 1

&lt;400&gt; 82 .

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
          20           25           30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val
          35           40           45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro
          50           55           60

```

```

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln
65           70           75           80

```

```

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro
          85           90           95

```

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
          100          105          110

```

```

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp
          115          120          125

```

```

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu
          130          135          140

```

```

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val
          145          150          155          160

```



Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys  
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
 580 585 590

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met  
 595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp  
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val

625		630		635		640
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg						
	645			650		655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala						
	660			665		670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu						
	675			680		685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys						
	690			695		700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly						
705		710		715		720
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu						
	725			730		735
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala						
	740			745		750
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met						
	755			760		765
Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala						
	770			775		780
Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu						
785		790		795		800
Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu						
	805			810		815
Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile						
	820			825		830
Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu						
	835			840		845
Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly Arg						
	850			855		860

Lys Lys Arg Arg Gln Arg Arg Arg  
865 870

<210> 83  
<211> 2619  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Rattus norvegicus and Human immunodeficiency virus type 1

<400> 83  
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gagagggtag tgtttgcccc agttcgcatg gtgaccgtcc cccacgcca ctactgcata 180  
gtggccaacc ctgtgtcccc ggacaccag agttctgtgt tatttgacat cacaggacaa 240  
gtccgactcc ggcacgctga ccaggagatc cgactagccc aggaccctt cccctgtat 300  
ccaggggagg tgctggaaaa ggacatcacc ccactgcagg tggttctgcc caacacagca 360  
ctgcatttta aggcgttgct ggactttgag gataagaatg gagacaaggt catggcagga 420  
gacgagtggc tatttgaggg acctggcacc tacatccac agaaggaagt ggaagtcgtg 480  
gagatcattc aggccacagt catcaaacag aaccaagcac tgcggctaag ggcccgaaag 540  
gagtgccttg accgggaggg caaggggagc gtgacaggtg aggagtggct ggtccgatcc 600  
gtgggggctt acctcccagc tgtctttgaa gaggtgctgg atctgggtga tgctgtgatc 660  
cttacagaaa agactgccct gcacctccg gctctgcaga acttcaggga ccttcgggga 720  
gtgctccacc gcaccgggga ggaatgggta gtgacagtgc aggacacaga agcccatgtt 780  
ccagatgtct atgaggaggt gcttggggta gtacccatca ccaccctggg acctcgacac 840  
tactgtgtca ttcttgacc aatgggacca gacggcaaga accagctggg acaaaagcgt 900  
gttgtcaagg gagagaagtc ctttttcctc cagccaggag agaggctgga gcgaggcatc 960  
caggatgtgt atgtgctgtc agagcagcag gggctgtac tgaaggcact gcagccctg 1020  
gaggagggag agagcgagga gaagggtctc catcaggccg gagactgctg gctcatccgt 1080  
gggcccctgg agtatgtgcc atctgcaaaa gtggaggtgg tggaggagcg tcaggctatc 1140  
cctctggacc aaaatgaggg catctatgtg caggatgtca agacggggaa ggtgcgggct 1200  
gtgattggaa gcacctacat gctgactcag gatgaagtc tgtgggaaaa ggagctgcct 1260  
tctgggggtg aggagctgct gaacttgggg catgaccctc tggcagacag gggtcagaag 1320  
ggcacagcca agcccttca gccctcagct ccaaggaaca agaccgagt ggtcagctac 1380

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cgtgtcccg c acaatgcagc ggtgcaggtc tatgactaca gagccaagag agcccgtgtg 1440
gtctttgggc c cgagctagt gacactggat cctgaggagc agttcacagt attgtccctt 1500
tctgccgggc g acccaagcg tcctcatgcc cgccgtgcac tctgcctact gctgggacct 1560
gatttcttta ctgatgtcat caccatcgaa actgcagatc atgccagggt gcagctgcag 1620
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aaggctcgag accaggcagt ctttcccaa aacgggctgg tagtcagcag tgtggatgtg 1920
cagtcagtgg agcccgtgga ccagaggacc cgggatgccc ttcagcgag cgttcagctg 1980
gccatcgaaa ttaccaccaa ctcccaggag gcagcagcca agcacgaggc tcagagactg 2040
gaacaggaag cccgtgggtcg gcttgagagg cagaagatct tggaccagtc agaagctgaa 2100
aaagcccgca aggaactctt ggagcttgag gctatgagca tggctgtgga gagcacgggt 2160
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gtgctgcagg ccaagctcaa ggcacaggcg ctagccattg agacggaggc tgagttggag 2280
cgagtaaaga aagtacgaga gatggaactg atctatgccc gggcccagtt ggagctggag 2340
gtgagcaagg cgcagcagct tgccaatgtg gaggcaaaga agttcaagga gatgacagag 2400
gcactggggc ccggcaccat cagggacctg gctgtggccg ggccagagat gcaggtgaaa 2460
cttctccagt ccctgggcct gaaatccact ctcatcaccg atggctcgtc tcccatcaac 2520
ctcttcagca cagccttcgg gttgctgggg ctggggtctg atggtcagcc gccagcacag 2580
aagtacgggc ggaagaagcg gcgacagagg cgacggtga 2619

```

&lt;210&gt; 84

&lt;211&gt; 179

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; completely synthesized

&lt;400&gt; 84

```

Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly
1           5           10           15

```

```

Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe

```

Ile Gly Arg

```
<220>
<223> completely synthesized
```

```
<400>      85
gacattgtgc tgaccaatc tccagcttct ttggctgtgt ctcttgggca gagggccacc      60
atgtcctgca gagccggtga aagtgttgat atttttggcg ttgggttttt gcaactggtac      120
cagcagaaac caggacagcc acccaaactc ctcatctatc gtgcatccaa cctagaatct      180
```

```

gggatccctg tcagggttcag tggcactggg tctaggacag acttcaccct catcattgat      240
cctgtggagg ctgatgatgt tgccacctat tactgtcagc aaactaatga ggatccgtac      300
acgttcggag gggggaccaa gctggaaata aaaggcagta ctagcggcgg tggctccggg      360
ggcggttccg gtgggggcgg cagcagcgag gttcagctac aacagtctgg ggcagagctt      420
gtggagccag gggcctcagt caagttgtcc tgcacagctt ctggcttcaa cattaaagac      480
acctatatgc actgggtgaa gcagaggcct gaacagggcc tggaatggat tggaaggatt      540
gatcctgcga atggtaatag taaatatgtc ccgaagttcc agggcaaggc cactataaca      600
gcagacacat cttccaacac agcctacctg cagctcacca gcctgacatc tgaggacact      660
gccgtctatt attgtgctcc gtttggttac tacgtgtctg actatgctat ggcctactgg      720
ggtcaaggaa cctcagtcac cgtctcg                                           747

```

<210> 86

<211> 1072

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 86

```

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1              5              10              15

```

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro
20              25              30

```

```

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met
35              40              45

```

```

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro
50              55              60

```

```

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln
65              70              75              80

```

```

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro
85              90              95

```

```

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu
100              105              110

```

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln  
 340 345 350



Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 530 535 540

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys  
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His

580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr 595 600 605		
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp 610 615 620		
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625 630 635 640		
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645 650 655		
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660 665 670		
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675 680 685		
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690 695 700		
Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly 705 710 715 720		
Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu 725 730 735		
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala 740 745 750		
Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu 755 760 765		
Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala 770 775 780		
Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu 785 790 795 800		
Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu 805 810 815		

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile Val  
 885 890 895

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala  
 900 905 910

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly  
 915 920 925

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu  
 930 935 940

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser  
 945 950 955 960

Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu  
 965 970 975

Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro  
 980 985 990

Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser  
 995 1000 1005

Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu  
 1010 1015 1020

Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala  
 1025 1030 1035

Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp  
 1040 1045 1050

I

Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu  
 1055 1060 1065

Trp Ile Gly Arg  
 1070

<210> 87  
 <211> 3429  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens

<400> 87  
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 cagaacagca acgtgtcccg tgtggaggtc gggccaaaga cctacatccg gcaggacaat 120  
 gagagggtac tgtttgcccc catgcgcata gtgaccgtcc cccacgtca ctactgcaca 180  
 gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgtttgatgt cacagggcaa 240  
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 ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caacactgcc 360  
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 gtaggggctg acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc 660  
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 gtgtcccgcc gactgggga ggagtggctg gtaacagtgc aggacacaga ggcccacgtg 780  
 ccagatgtcc acgaggaggt gctgggggtt gtgccatca ccaccctggg ccccccacaac 840  
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gccatcgaga tcaccaccaa ctcccaggaa gcggcggcca agcatgaggc tcagagactg 2040  
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gccacctatt actgtcagca aactaatgag gatccgtaca cgttcggagg ggggaccaag 3000  
 ctggaaataa aaggcagtac tagcggcggt ggctccgggg gcggttccgg tgggggcggc 3060  
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 aagttgtcct gcacagcttc tggcttcaac attaaagaca cctatatgca ctgggtgaag 3180  
 cagaggcctg aacagggcct ggaatggatt ggaaggattg atcctgcgaa tggtaatagt 3240  
 aaatatgtcc cgaagttcca gggcaaggcc actataacag cagacacatc ttccaacaca 3300  
 gcctacctgc agctcaccag cctgacatct gaggacactg ccgtctatta ttgtgtccg 3360  
 tttggttact acgtgtctga ctatgctatg gcctactggg gtcaaggaac ctcagtcacc 3420  
 gtctcgtga 3429

<210> 88  
 <211> 1040  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Rattus norvegicus

<400> 88

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 1 5 10 15

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp

115	120	125
Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu 130	135	140
Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val 145	150	155 160
Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu 165	170	175
Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr 180	185	190
Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val 195	200	205
Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys 210	215	220
Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly 225	230	235 240
Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr 245	250	255
Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro 260	265	270
Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met 275	280	285
Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly 290	295	300
Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile 305	310	315 320
Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala 325	330	335
Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln 340	345	350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 500 505 510

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 515 520 525

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 530 535 540

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys  
 545 550 555 560

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 565 570 575

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
 580 585 590



Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met  
 595 600 605

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp  
 610 615 620

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
 625 630 635 640

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
 645 650 655

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
 660 665 670

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
 675 680 685

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
 690 695 700

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly  
 705 710 715 720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
 725 730 735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met  
 755 760 765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 770 775 780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
 785 790 795 800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile

820	825	830
Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu 835 840 845		
Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile Val 850 855 860		
Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala 865 870 875 880		
Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly 885 890 895		
Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu 900 905 910		
Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe Ser 915 920 925		
Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val Glu 930 935 940		
Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro 945 950 955 960		
Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser 965 970 975		
Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Val 980 985 990		
Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val 995 1000 1005		
Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr 1010 1015 1020		
Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile 1025 1030 1035		
Gly Arg 1040		

<210> 89  
 <211> 3333  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized and *Rattus norvegicus*

<400> 89  
 atggcaactg aagaggccat catccgcac ccccatacc actacatcca tgtgctggac 60  
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 gagagggtac tgtttgcccc agttcgcatg gtgaccgtcc cccacgcca ctactgcata 180  
 gtggccaacc ctgtgtcccg ggacaccag agttctgtgt tatttgacat cacaggacaa 240  
 gtccgactcc ggcacgctga ccaggagatc cgactagccc aggaccctt cccctgtat 300  
 ccaggggagg tgctggaaaa ggacatcacc cactgcagg tggttctgcc caacacagca 360  
 ctgcatctta aggcgttgct ggactttgag gataagaatg gagacaagg catggcagga 420  
 gacgagtggc tatttgaggg acctggcacc tacatccac agaaggaagt ggaagtcgtg 480  
 gagatcattc aggccacagt catcaaacag aaccaagcac tgcggctaag ggcccgaag 540  
 gagtgctttg accgggaggg caaggggagc gtgacagggt aggagtggct ggtccgatcc 600  
 gtgggggctt acctccagc tgtctttgaa gaggtgctgg atctgggtga tgctgtgatc 660  
 cttacagaaa agactgccct gcacctccg gctctgcaga acttcaggga cttcggggga 720  
 gtgctccacc gcaccgggga ggaatggtta gtgacagtgc aggacacaga agcccatggt 780  
 ccagatgtct atgaggaggt gcttggggta gtacctatca ccacctggg acctcgacac 840  
 tactgtgtca ttcttgacct aatgggacca gacggcaaga accagctggg acaaaagcgt 900  
 gttgtcaagg gagagaagtc ctttttcctc cagccaggag agaggctgga gcgaggcatc 960  
 caggatgtgt atgtgctgtc agagcagcag gggctgctac tgaaggcact gcagcccctg 1020  
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 gggcccctgg agtatgtgcc atctgcaaaa gtggagggtg tggaggagcg tcaggctatc 1140  
 cctctggacc aaaatgaggg catctatgtg caggatgtca agacggggaa ggtgcgggct 1200  
 gtgattggaa gcacctacat gctgactcag gatgaagtcc tgtgggaaaa ggagctgcct 1260  
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 cgtgtcccg acaatgcagc ggtgcaggct tatgactaca gagccaagag agcccgtgtg 1440  
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tctgccgggc gacccaagcg tcctcatgcc cgccgtgcac tctgcctact gctgggacct	1560
gattttcttta ctgatgtcat caccatcgaa actgcagatc atgccagggtt gcagctgcag	1620
cttgectaca actggcactt tgaactgaag aaccggaatg accctgcaga ggcagccaag	1680
cttttctccg tgcctgactt cgtgggtgac gcctgcaagg ccattgcatc ccgagtccgg	1740
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atggctgttt ttggctttga gatgtctgaa gacacaggtc ctgatggcac actcctgccc	1860
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cagtcagtgg agcccgtgga ccagaggacc cgggatgccc ttcagcgcag cgttcagctg	1980
gccatcgaaa ttaccaccaa ctcccaggag gcagcagcca agcacgaggc tcagagactg	2040
gaacaggaag cccgtggtcg gcttgagagg cagaagatct tggaccagtc agaagctgaa	2100
aaagcccgca aggaactctt ggagcttgag gctatgagca tggctgtgga gagcacgggt	2160
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gtgctgcagg ccaagctcaa ggcacaggcg ctagccattg agacggaggc tgagttggag	2280
cgagtaaaga aagtacgaga gatggaactg atctatgccc gggcccagtt ggagctggag	2340
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taccagcaga aaccaggaca gccacccaaa ctctcatct atcgtgcatc caacctagaa	2760
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gatcctgtgg aggctgatga tgttgccacc tattactgtc agcaaactaa tgaggatccg	2880
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gacacctata tgcactgggt gaagcagagg cctgaacagg gcctggaatg gattggaagg	3120
attgatcctg cgaatggtaa tagtaaatat gtcccgaagt tccagggcaa ggccactata	3180
acagcagaca catcttccaa cacagcctac ctgcagctca ccagcctgac atctgaggac	3240

actgccgtct attattgtgc tccgtttggt tactacgtgt ctgactatgc tatggcctac 3300  
 tgggggtcaag gaacctcagt caccgtctcg tga 3333

<210> 90  
 <211> 56  
 <212> PRT  
 <213> Homo sapiens

<400> 90

Met Gly Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys  
 1 5 10 15

Leu His Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala  
 20 25 30

Cys Asn Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp  
 35 40 45

Leu Lys Trp Trp Glu Leu Arg Ala  
 50 55

<210> 91  
 <211> 171  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
 atgggtaact ctgactccga atgcccgctg tctcagcagc gttattgcct gcatgatggg 60  
 gtttgtatgt atatcgaagc tctggacaaa tatgcttgca actgtgttgt tggttacatc 120  
 ggtgagcggt gccagtatcg cgacctgaaa tgggtgggaac tgcgtgcatg a 171

<210> 92  
 <211> 949  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Synthesized from two Homo sapiens sequences

<400> 92

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 1 5 10 15

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 50 55 60

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 65 70 75 80

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 115 120 125

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 145 150 155 160

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 225 230 235 240

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln  
 340 345 350

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
 435 440 445

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
 485 490 495

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg

500	505	510
Ala Leu Cys Leu Leu Leu Gly	Pro Asp Phe Phe Thr Asp	Val Ile Thr
515	520	525
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn		
530	535	540
Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys		
545	550	555 560
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala		
565	570	575
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His		
580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr		
595	600	605
Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp		
610	615	620
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val		
625	630	635 640
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg		
645	650	655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala		
660	665	670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu		
675	680	685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys		
690	695	700
Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly		
705	710	715 720
Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu		
725	730	735



Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
 740 745 750

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
 755 760 765

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 770 775 780

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
 785 790 795 800

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 805 810 815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 820 825 830

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
 835 840 845

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 850 855 860

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
 865 870 875 880

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly Asn  
 885 890 895

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp  
 900 905 910

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys  
 915 920 925

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp  
 930 935 940

Trp Glu Leu Arg Ala  
 945

<210> 93  
 <211> 2850

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthesized from two Homo sapiens sequences

&lt;400&gt; 93

atggcaactg aagagttcat catccgcac ccccatacc actatatcca tgtgctggac	60
cagaacagca acgtgtcccg tgtggaggtc gggccaaaga cctacatccg gcaggacaat	120
gagaggggtac tgtttgcccc catgcgcacg gtgaccgtcc cccacgtca ctactgcaca	180
gtggccaacc ctgtgtctcg ggatgccag ggcttggtgc tgttgatgt cacagggcaa	240
gttcggcttc gccacgtga cctcgagac cggctggccc aggaccctt cccctgtac	300
ccaggggagg tgctggaaaa ggacatcaca cccctgcagg tggttctgcc caacactgcc	360
ctccatctaa aggcgctgct tgattttgag gataaagatg gagacaaggt ggtggcagga	420
gatgagtggc ttttcgaggg acctggcacg tacatcccc ggaaggaagt ggaggtcgtg	480
gagatcattc aggccaccat catcaggcag aaccaggctc tgcggctcag ggcccgcaag	540
gagtgctggg accgggacgg caaggagagg gtgacagggg aagaatggct ggtcaccaca	600
gtaggggctg acctcccagc ggtgtttgag gaggttctgg atttggtgga cgccgtcatc	660
cttacggaaa agacagccct gcacctcgg gctcggcgga acttcggga cttcagggga	720
gtgtcccgcc gactgggga ggagtggctg gtaacagtgc aggacacaga ggccacgtg	780
ccagatgtcc acgaggaggt gctgggggtt gtgcccata ccacctggg ccccccacaac	840
tactgcgtga ttctcgacc tgctggaccg gatggcaaga atcagctggg gcagaagcgc	900
gtggtcaagg gagagaagtc ttttttcctc cagccaggag agcagctgga acaaggcatc	960
caggatgtgt atgtgctgtc ggagcagcag gggctgctgc tgagggccct gcagcccctg	1020
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ggaccccctg agtatgtgcc atctgcaaaa gtggaggtgg tggaggagcg ccaggccatc	1140
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gtgattggaa gcacctacat gctgaccag gacgaagtcc tgtgggagaa agagctgcct	1260
cccgggggtg aggagctgct gaacaagggg caggaccctc tggcagacag gggtgagaag	1320
gacacagcta agagcctcca gcccttggcg ccccggaaca agaccgtgt ggtcagctac	1380
cgcggtgccc acaacgctgc ggtgcaggtg tacgactacc gagagaagcg agcccgctg	1440
gtcttcgggc ctgagctggg gtcgctgggt cctgaggagc agttcacagt gttgtccctc	1500
tcagctgggc ggccaagcg tccccatgcc cgcgtgcgc tctgcctgct gctggggcct	1560

```

gactttcttca cagacgtcat caccatcgaa acggcggatc atgccaggct gcaactgcag 1620
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ctcttttcag tgccagactt tgtaggtgat gcctgcaaag ccatcgcatc ccgggtgcgg 1740
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gtgctgcagg ccaagctaaa agcacaggcc ttggccattg aaacggaggc tgagctccag 2280
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ctggacaaat atgcttgcaa ctgtgttgtt ggttacatcg gtgagcgttg ccagtatcgc 2820
gacctgaaat ggtgggaact gcgtgcatga 2850

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&lt;210&gt; 94

&lt;211&gt; 917

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Rattus norvegicus and Homo sapiens

&lt;400&gt; 94

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
1           5           10           15

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 20 25 30

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
 35 40 45

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
 50 55 60

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
 65 70 75 80

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
 85 90 95

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 100 105 110

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 115 120 125

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
 130 135 140

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
 145 150 155 160

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 165 170 175

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 180 185 190

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 195 200 205

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 210 215 220

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
 225 230 235 240

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 245 250 255

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
 260 265 270

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met  
 275 280 285

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 290 295 300

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile  
 305 310 315 320

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
 325 330 335

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
 340 345 350

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 355 360 365

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln  
 370 375 380

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 385 390 395 400

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 405 410 415

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
 420 425 430

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
 435 440 445

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 450 455 460

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val  
 465 470 475 480

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr

485	490	495
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg 500	505	510
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr 515	520	525
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn 530	535	540
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys 545	550	555
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 565	570	575
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His 580	585	590
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met 595	600	605
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp 610	615	620
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 625	630	635
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 645	650	655
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 660	665	670
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 675	680	685
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 690	695	700
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 705	710	715
		720

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
                   725                  730                  735

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
                   740                  745                  750

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met  
                   755                  760                  765

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
                   770                  775                  780

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
                   785                  790                  795                  800

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
                   805                  810                  815

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
                   820                  825                  830

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
                   835                  840                  845

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly Asn  
                   850                  855                  860

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp  
                   865                  870                  875                  880

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys  
                   885                  890                  895

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp  
                   900                  905                  910

Trp Glu Leu Arg Ala  
                   915

<210> 95

<211> 2754

<212> DNA

<213> Artificial Sequence

<220>

&lt;223&gt; Rattus norvegicus and Homo sapiens

&lt;400&gt; 95

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cagaacagta atgtgtcccc tgtggagggt ggaccaaaga cctacatccg gcaggacaat	120
gagaggggtac tgtttgcccc agttcgcata gtgaccgtcc cccacgcca ctactgcata	180
gtggccaacc ctgtgtcccc ggacaccag agttctgtgt tatttgacat cacaggacaa	240
gtccgactcc ggcacgtga ccaggagatc cgactagccc aggaccctt cccctgtat	300
ccaggggagg tgctggaaaa ggacatcacc cactgcagg tggttctgcc caacacagca	360
ctgcatctta aggcgttgct ggactttgag gataagaatg gagacaaggt catggcagga	420
gacgagtggc tatttgaggg acctggcacc tacatcccac agaaggaagt ggaagtcgtg	480
gagatcattc aggccacagt catcaaacag aaccaagcac tgcggctaag ggcccgaag	540
gagtgccttg accgggaggg caaggggccc gtgacaggtg aggagtggct ggtccgatcc	600
gtgggggctt acctccagc tgtcttgaa gaggtgctgg atctgggtga tgctgtgatc	660
cttacagaaa agactgcct gcacctccg gctctgcaga acttcaggga ccttcgggga	720
gtgctccacc gcaccgggga ggaatggta gtgacagtgc aggacacaga agcccatggt	780
ccagatgtct atgaggaggt gcttggggta gtacctca ccacctggg acctcgacac	840
tactgtgtca ttcttgacc aatgggacca gacggcaaga accagctggg acaaaagcgt	900
gttgtcaagg gagagaagtc ctttttcctc cagccaggag agaggctgga gcgaggcatc	960
caggatgtgt atgtgctgtc agagcagcag gggctgctac tgaaggcact gcagcccctg	1020
gaggagggag agagcgagga gaaggtctcc catcaggccg gagactgctg gctcatccgt	1080
gggcccctgg agtatgtgcc atctgcaaaa gtggaggtgg tggaggagcg tcaggctatc	1140
cctctggacc aaaatgaggg catctatgtg caggatgtca agacggggaa ggtgcgggct	1200
gtgattggaa gcacctacat gctgactcag gatgaagtcc tgtgggaaaa ggagctgcct	1260
tctgggggtg aggagctgct gaacttggg catgaccctc tggcagacag ggtcagaag	1320
ggcacagcca agccccttca gccctcagct ccaaggaaca agaccgagt ggtcagctac	1380
cgtgtcccc acaatgcagc ggtgcaggtc tatgactaca gagccaagag agcccgtgtg	1440
gtctttgggc ccgagctagt gacactggat cctgaggagc agttcacagt attgtccctt	1500
tctgccgggc gaccaagcg tcctcatgcc cgccgtgcac tctgcctact gctgggacct	1560
gatttcttta ctgatgtcat caccatcgaa actgcagatc atgccagggt gcagctgcag	1620
cttgccctaca actggcactt tgaactgaag aaccggaatg accctgcaga ggcagccaag	1680



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cttttctccg tgcctgactt cgtgggtgac gcctgcaagg ccattgcatc ccgagtcogg 1740
ggggctgtag cctctgtcac ctttgatgac ttccataaaa actcagcccg gatcattoga 1800
atggctgttt ttggctttga gatgtctgaa gacacaggtc ctgatggcac actcctgccc 1860
aaggctcgag accaggcagt ctttcccca aacgggctgg tagtcagcag tgtggatgtg 1920
cagtcagtgg agcccgtgga ccagaggacc cgggatgccc ttcagcgcag cgttcagctg 1980
gccatcga aa ttaccaccaa ctcccaggag gcagcagcca agcacgaggc tcagagactg 2040
gaacaggaag cccgtggctg gcttgagagg cagaagatct tggaccagtc agaagctgaa 2100
aaagcccga aggaactctt ggagcttgag gctatgagca tggctgtgga gagcacgggt 2160
aatgccaaag cagaggctga gtcccgtgca gaggcagcga ggatcgaagg agaaggctct 2220
gtgctgcagg ccaagctcaa ggcacaggcg ctagccattg agacggaggc tgagttggag 2280
cgagtaaaga aagtacgaga gatggaactg atctatgcc gggcccagtt ggagctggag 2340
gtgagcaagg cgcagcagct tgccaatgtg gaggcaaaga agttcaagga gatgacagag 2400
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cttctccagt ccctgggcct gaaatccact ctcatcaccg atggctcgtc tcccatcaac 2520
ctcttcagca cagccttcgg gttgctgggg ctgggggtctg atggtcagcc gccagcacag 2580
aagatgggta actctgactc cgaatgcccg ctgtctcagc acggttattg cctgcatgat 2640
gggtgtttgta tgtatatcga agctctggac aaatatgctt gcaactgtgt tgttggttac 2700
atcggtgagc gttgccagta tcgcgacctg aaatgggtggg aactgcgtgc atga 2754

```

&lt;210&gt; 96

&lt;211&gt; 1005

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> *Saccaromyces cerevisiae* and *Homo sapiens* and *Drosophila melanogaster*

&lt;400&gt; 96

```

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
1           5           10          15

```

```

Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20          25          30

```

```

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35          40          45

```

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr

275	280	285
Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val		
290	295	300
Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys		
305	310	315
Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly		
325	330	335
Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr		
340	345	350
Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro		
355	360	365
Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val		
370	375	380
Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly		
385	390	395
Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile		
405	410	415
Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala		
420	425	430
Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln		
435	440	445
Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser		
450	455	460
Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu		
465	470	475
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala		
485	490	495
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu		
500	505	510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
 530 535 540

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
 565 570 575

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 625 630 635 640

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys  
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr  
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp  
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly  
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Arg Gln Ile

980

985

990

Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys  
 995 1000 1005

<210> 97  
 <211> 3018  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> *Saccaromyces cerevisiae* and *Homo sapiens* and *Drosophila melanogaster*

<400> 97  
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 tgctccaaag aaaaaccgaa gtgcgccaag tgtctgaaga acaactggga gtgtcgctac 120  
 tctcccaaaa ccaaaggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180  
 ctagaaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240  
 ttgaaaatgg attctttaca ggatataaaa gcattgttaa caggattaat ggcaactgaa 300  
 gagttcatca tccgcatccc cccataccac tatatccatg tgctggacca gaacagcaac 360  
 gtgtcccgtg tggaggtcgg gccaaagacc tacatccggc aggacaatga gaggggtactg 420  
 tttgccccca tgcgcatggt gaccgtcccc ccacgtcact actgcacagt ggccaaccct 480  
 gtgtctcggg atgccaggg cttggtgctg tttgatgtca cagggaagt tccgcttcgc 540  
 cacgtgacc tcgagatccg gctggcccag gacccttcc ccctgtacct aggggaggtg 600  
 ctggaaaagg acatcacacc cctgcagggt gttctgcca aactgcct ccatctaaag 660  
 gcgctgcttg attttgagga taaagatgga gacaagggtg tggcaggaga tgagtggctt 720  
 ttcgagggaac ctggcacgta catcccccg aaggaagtgg aggtcgtgga gatcattcag 780  
 gccaccatca tcaggcagaa ccaggctctg cggctcaggg cccgcaagga gtgctgggac 840  
 cgggacggca aggagagggg gacaggggaa gaatggctgg tcaccacagt aggggcgtac 900  
 ctcccagcgg tgtttgagga ggttctggat ttggtggacg ccgtcatcct tacggaaaag 960  
 acagccctgc acctccgggc tcggcggaac ttccgggact tcaggggagt gtcccgcgcg 1020  
 actggggagg agtggctggt aacagtgcag gacacagagg cccacgtgcc agatgtccac 1080  
 gaggaggtgc tgggggttgt gcccatcacc accctgggccc cccacaacta ctgcgtgatt 1140  
 ctcgaccctg tcggaccgga tggcaagaat cagctggggc agaagcgcgt ggtcaagggg 1200  
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3018

<210> 98  
 <211> 973  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Drosophila melanogaster*

<400> 98

Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu  
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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
 165 170 175



Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
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Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met  
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile  
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
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Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
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Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
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Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln  
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
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Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
 515 520 525

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
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Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
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Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val  
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr  
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 625 630 635 640

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys

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Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 660 665 670		
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Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met 690 695 700		
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp 705 710 715 720		
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val 725 730 735		
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg 740 745 750		
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala 755 760 765		
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu 770 775 780		
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys 785 790 795 800		
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly 805 810 815		
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu 820 825 830		
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala 835 840 845		
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met 850 855 860		
Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala 865 870 875 880		

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
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Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
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Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
                     915                    920                    925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
                     930                    935                    940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Arg Gln Ile  
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Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys  
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<210> 99

<211> 2922

<212> DNA

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Drosophila melanogaster*

<400> 99

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<210> 100

<211> 1238

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and *Saccharomyces cerevisiae* and *Homo sapiens*

<400> 100

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
85 90 95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 165 170 175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln  
 435 440 445

Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu  
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 500 505 510

Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp  
 515 520 525

Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
 530 535 540

Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
 565 570 575

Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg



595

600

605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 625 630 635 640

Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys  
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr  
 690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp  
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly  
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Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
 850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
 885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
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Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
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Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile Val  
 980 985 990

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala  
 995 1000 1005

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val  
 1010 1015 1020

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys  
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Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val  
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Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile  
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Asp Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln  
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 Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu  
 1085 1090 1095  
 Ile Lys Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly  
 1100 1105 1110  
 Gly Gly Gly Ser Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu  
 1115 1120 1125  
 Leu Val Glu Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser  
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 Gly Phe Asn Ile Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg  
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 Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn  
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 Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile  
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 Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser  
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&lt;210&gt; 101

&lt;211&gt; 3717

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthesized and *Saccharomyces cerevisiae* and *Homo sapiens*

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<212> PRT

<213> Artificial Sequence

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<223> synthesized and *Saccharomyces cerevisiae* and *Rattus norvegicus*

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Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 340 345 350

Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro  
 355 360 365

Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met  
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile  
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala  
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln  
 435 440 445

Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser  
 450 455 460

Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln  
 465 470 475 480

Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala  
 485 490 495

Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
 500 505 510

Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp  
 515 520 525

Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro  
 530 535 540

Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
 545 550 555 560

Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val  
 565 570 575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr  
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn



625	630	635	640
Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys	645	650	655
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala	660	665	670
Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His	675	680	685
Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met	690	695	700
Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp	705	710	715
Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val	725	730	735
Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg	740	745	750
Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala	755	760	765
Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu	770	775	780
Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys	785	790	795
Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly	805	810	815
Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu	820	825	830
Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala	835	840	845
Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met	850	855	860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile Val  
 945 950 955 960

Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg Ala  
 965 970 975

Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val Gly  
 980 985 990

Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu Leu  
 995 1000 1005

Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe  
 1010 1015 1020

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro  
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Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn  
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Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys  
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Gly Ser Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly  
 1070 1075 1080

Gly Ser Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val  
 1085 1090 1095

Glu Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe  
 1100 1105 1110

Asn Ile Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu  
 1115 1120 1125

Gln Gly Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn  
 1130 1135 1140

Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala  
 1145 1150 1155

Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr  
 1160 1165 1170

Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr  
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Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr Ser Val  
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Thr Val Ser  
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<210> 103  
 <211> 3621  
 <212> DNA  
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<220>  
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<210> 104

<211> 1045

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and two *Homo sapiens* sequences

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 35 40 45  
 Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60  
 Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80  
 Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95  
 Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 100 105 110  
 His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125  
 Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
 130 135 140  
 Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
 145 150 155 160  
 Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
 165 170 175  
 Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190  
 Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205  
 Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220  
 Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 225 230 235 240



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 Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu  
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 Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro  
                                  530                                   535                                   540  
 Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His  
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 Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val  
                                  565                                   570                                   575  
 Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr  
                                  580                                   585                                   590  
 Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
                                  595                                   600                                   605  
 Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
                                  610                                   615                                   620  
 Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
                                  625                                   630                                   635                                   640  
 Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys  
                                  645                                   650                                   655  
 Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
                                  660                                   665                                   670  
 Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
                                  675                                   680                                   685  
 Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr  
                                  690                                   695                                   700



Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp  
705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly  
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly Asn  
 980 985 990

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp  
 995 1000 1005

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn  
 1010 1015 1020

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu  
 1025 1030 1035

Lys Trp Trp Glu Leu Arg Ala  
 1040 1045

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<220>  
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<210> 106

<211> 1013

<212> PRT

<213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Homo sapiens*

<400> 106

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 20 25 30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
 35 40 45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
 50 55 60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
 65 70 75 80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
 85 90 95

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
 100 105 110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320



545	550	555	560
Asn Ala Ala Val	Gln Val Tyr Asp Tyr	Arg Ala Lys Arg Ala	Arg Val
	565	570	575
Val Phe Gly Pro	Glu Leu Val Thr	Leu Asp Pro Glu	Glu Gln Phe Thr
	580	585	590
Val Leu Ser Leu	Ser Ala Gly Arg	Pro Lys Arg Pro	His Ala Arg Arg
	595	600	605
Ala Leu Cys Leu	Leu Leu Gly Pro	Asp Phe Phe Thr	Asp Val Ile Thr
	610	615	620
Ile Glu Thr Ala	Asp His Ala Arg	Leu Gln Leu Gln	Leu Ala Tyr Asn
	625	630	635
Trp His Phe Glu	Leu Lys Asn Arg	Asn Asp Pro Ala	Glu Ala Ala Lys
	645	650	655
Leu Phe Ser Val	Pro Asp Phe Val	Gly Asp Ala Cys	Lys Ala Ile Ala
	660	665	670
Ser Arg Val Arg	Gly Ala Val Ala	Ser Val Thr Phe	Asp Asp Phe His
	675	680	685
Lys Asn Ser Ala	Arg Ile Ile Arg	Met Ala Val Phe	Gly Phe Glu Met
	690	695	700
Ser Glu Asp Thr	Gly Pro Asp Gly	Thr Leu Leu Pro	Lys Ala Arg Asp
	705	710	715
Gln Ala Val Phe	Pro Gln Asn Gly	Leu Val Val Ser	Ser Val Asp Val
	725	730	735
Gln Ser Val Glu	Pro Val Asp Gln	Arg Thr Arg Asp	Ala Leu Gln Arg
	740	745	750
Ser Val Gln Leu	Ala Ile Glu Ile	Thr Thr Asn Ser	Gln Glu Ala Ala
	755	760	765
Ala Lys His Glu	Ala Gln Arg Leu	Glu Gln Glu Ala	Arg Gly Arg Leu
	770	775	780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly  
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
 820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
 835 840 845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met  
 850 855 860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
 865 870 875 880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
 885 890 895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
 900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 915 920 925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
 930 935 940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Met Gly Asn  
 945 950 955 960

Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His Asp  
 965 970 975

Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn Cys  
 980 985 990

Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys Trp  
 995 1000 1005

Trp Glu Leu Arg Ala  
 1010



<210> 107  
 <211> 3042  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> *Saccaromyces cerevisiae* and *Rattus norvegicus* and *Homo sapiens*

<400> 107

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<210> 108
<211> 1000
<212> PRT

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## &lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> *Saccaromyces cerevisiae* and *Homo sapiens* and Human immunodeficiency virus type 1

&lt;400&gt; 108

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu  
                     20                      25                      30

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro  
                     35                      40                      45

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu  
                     50                      55                      60

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile  
                     65                      70                      75                      80

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu  
                     85                      90                      95

Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile  
                     100                      105                      110

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
                     115                      120                      125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Met  
                     130                      135                      140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn Pro  
                     145                      150                      155                      160

Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly Gln  
                     165                      170                      175

Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp Pro  
                     180                      185                      190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
                     195                      200                      205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg Gly  
 325 330 335

Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr  
 340 345 350

Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val Pro  
 355 360 365

Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro Val  
 370 375 380

Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly  
 385 390 395 400

Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly Ile  
 405 410 415

Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg Ala  
 420 425 430

Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His Gln

435	440	445
Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser 450 455 460		
Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Glu 465 470 475 480		
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala 485 490 495		
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu 500 505 510		
Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln Asp 515 520 525		
Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln Pro 530 535 540		
Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His 545 550 555 560		
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg Val 565 570 575		
Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe Thr 580 585 590		
Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg 595 600 605		
Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr 610 615 620		
Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn 625 630 635 640		
Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala Lys 645 650 655		
Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala 660 665 670		

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu Thr  
690 695 700

Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg Asp  
705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr Gly  
805 810 815

Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
820 825 830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
835 840 845

Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu Leu  
850 855 860

Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
865 870 875 880

Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr Glu  
885 890 895

Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
900 905 910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
 915 920 925

Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly Leu  
 930 935 940

Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala Ser  
 945 950 955 960

Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala Pro  
 965 970 975

Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly Arg  
 980 985 990

Lys Lys Arg Arg Gln Arg Arg Arg  
 995 1000

<210> 109  
 <211> 3003  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> *Saccaromyces cerevisiae* and *Homo sapiens* and Human  
 immunodeficiency virus type 1

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accaccaact cccaggaagc ggcgggccaag catgaggctc agagactgga gcaggaagcc	2340
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gaggccgagt cccgtgcgga ggcagcccg attgagggag aaggggccgt gctgcaggcc 2520
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<210> 110
<211> 968
<212> PRT
<213> Artificial Sequence

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<220>
<223> Saccharomyces cerevisiae and Rattus norvegicus and Human
immunodeficiency virus type 1

```

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<400> 110

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Met Lys Leu Leu Ser Ser Ile Glu Gln Ala Cys Asp Ile Cys Arg Leu
1           5           10           15

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Lys Lys Leu Lys Cys Ser Lys Glu Lys Pro Lys Cys Ala Lys Cys Leu
20           25           30

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```

Lys Asn Asn Trp Glu Cys Arg Tyr Ser Pro Lys Thr Lys Arg Ser Pro
35           40           45

```

```

Leu Thr Arg Ala His Leu Thr Glu Val Glu Ser Arg Leu Glu Arg Leu
50           55           60

```

```

Glu Gln Leu Phe Leu Leu Ile Phe Pro Arg Glu Asp Leu Asp Met Ile
65           70           75           80

```

```

Leu Lys Met Asp Ser Leu Gln Asp Ile Lys Ala Leu Leu Thr Gly Leu
85           90           95

```

```

Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr Ile
100          105          110

```

His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly Pro  
 115 120 125

Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro Val  
 130 135 140

Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn Pro  
 145 150 155 160

Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly Gln  
 165 170 175

Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp Pro  
 180 185 190

Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro Leu  
 195 200 205

Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu Asp  
 210 215 220

Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp Leu  
 225 230 235 240

Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val Val  
 245 250 255

Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg Leu  
 260 265 270

Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val Thr  
 275 280 285

Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala Val  
 290 295 300

Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu Lys  
 305 310 315 320

Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg Gly  
 325 330 335

Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp Thr

340	345	350
Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val Pro		
355	360	365
Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro Met		
370	375	380
Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys Gly		
385	390	395
400		
Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly Ile		
405	410	415
Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys Ala		
420	425	430
Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His Gln		
435	440	445
Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro Ser		
450	455	460
Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp Gln		
465	470	475
480		
Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg Ala		
485	490	495
Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp Glu		
500	505	510
Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His Asp		
515	520	525
Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln Pro		
530	535	540
Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro His		
545	550	555
560		
Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg Val		
565	570	575

Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe Thr  
 580 585 590

Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg Arg  
 595 600 605

Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile Thr  
 610 615 620

Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr Asn  
 625 630 635 640

Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala Lys  
 645 650 655

Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile Ala  
 660 665 670

Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe His  
 675 680 685

Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu Met  
 690 695 700

Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg Asp  
 705 710 715 720

Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp Val  
 725 730 735

Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln Arg  
 740 745 750

Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala Ala  
 755 760 765

Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg Leu  
 770 775 780

Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg Lys  
 785 790 795 800

Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr Gly  
 805 810 815

Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile Glu  
                   820                                  825                                  830

Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu Ala  
                   835                                  840                                  845

Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu Met  
           850                                  855                                  860

Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys Ala  
   865                                  870                                  875                                  880

Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr Glu  
                                   885                                  890                                  895

Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro Glu  
                                   900                                  905                                  910

Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu Ile  
                   915                                  920                                  925

Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly Leu  
   930                                  935                                  940

Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly Arg  
   945                                  950                                  955                                  960

Lys Lys Arg Arg Gln Arg Arg Arg  
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<210> 111

<211> 2907

<212> DNA

<213> Artificial Sequence

<220>

<223> Saccharomyces cerevisiae and Rattus norvegicus and Human  
           immunodeficiency virus type 1

<400> 111

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tctcccaaaa ccaaaagggtc tccgctgact agggcacatc tgacagaagt ggaatcaagg 180

ctagaaagac tggaacagct atttctactg atttttcctc gagaagacct tgacatgatt 240

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<210> 112  
 <211> 1040  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Homo sapiens and Drosophila melanogaster

<400> 112

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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr  
130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu  
145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe  
165 170 175

Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val  
180 185 190

Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val  
195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala  
210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile  
225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala  
245 250 255

Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp  
260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val  
275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala  
290 295 300



Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp  
 355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu  
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro  
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys  
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val

530	535	540
Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys		
545	550	555 560
Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser		
	565	570 575
Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg		
	580	585 590
Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg		
	595	600 605
Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu		
	610	615 620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His		
	625	630 635 640
Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp		
	645	650 655
Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu		
	660	665 670
Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu		
	675	680 685
Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
	690	695 700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
	705	710 715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly		
	725	730 735
Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg		
	740	745 750
Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
	755	760 765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala  
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln  
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg  
 805 810 815

Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys  
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu  
 835 840 845

Ser Thr Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala  
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln  
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val  
 885 890 895

Arg Glu Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val  
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln  
 915 920 925

Met Thr Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala  
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser  
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala  
 965 970 975

Phe Gly Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg  
 980 985 990

Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala  
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu  
 1010 1015 1020

Arg Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp  
 1025 1030 1035

Lys Lys  
 1040

<210> 113  
 <211> 3123  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Homo sapiens and Drosophila melanogaster

<400> 113  
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gacttccata agaactcagc ccgcatcatt cgcactgctg tctttggctt tgagacctcg 2220  
gaagcgaagg gccccgatgg catggccctg ccaggccccc gggaccaggc tgtcttcccc 2280  
caaaacgggc tgggtgtcag cagtgtggac gtgcagtcag tggagcctgt ggatcagagg 2340  
acccgggacg ccctgcaacg cagcgtccag ctggccatcg agatcaccac caactccag 2400  
gaagcggcgg ccaagcatga ggctcagaga ctggagcagg aagcccgcgg ccggcttgag 2460  
cggcagaaga tcctggacca gtcagaagcc gagaaagctc gcaaggaact tttggagctg 2520  
gaggctctga gcatggccgt ggagagcacc gggactgccg aggcggaggc cgagtcccg 2580  
gcggaggcag cccggattga gggagaaggg tccgtgctgc aggccaagct aaaagcacag 2640  
gccttggcca ttgaaacgga ggctgagctc cagaggggtcc agaagggtccg agagctggaa 2700  
ctggtctatg cccgggcccga gctggagctg gaggtgagca aggctcagca gctggctgag 2760  
gtggaggatga agaagttcaa gcagatgaca gaggccatag gcccagcac catcagggac 2820

```

cttgctgtgg ctgggcctga gatgcaggta aaactgctcc agtccctggg cctgaaatca 2880
accctcatca cccgatggctc cactcccatc aacctcttca acacagcctt tgggctgctg 2940
gggatggggc cccaggggtca gcccctgggc agaaggggtgg ccagtggggc cagccctggg 3000
gaggggatat ccccccagtc tgctcaggcc cctcaagctc ctggagacaa ccacgtggtg 3060
cctgtactgc gccgacagat caagatctgg ttccagaacg cacggatgaa gtggaagaag 3120
tga 3123

```

&lt;210&gt; 114

&lt;211&gt; 1008

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Levivirus and Rattus norvegicus and Drosophila melanogaster

&lt;400&gt; 114

```

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10           15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
          20           25           30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
          35           40           45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
          50           55           60

```

```

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
          65           70           75           80

```

```

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
          85           90           95

```

```

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
          100          105          110

```

```

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
          115          120          125

```

```

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr
          130          135          140

```

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu  
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe  
 165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val  
 180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile  
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala  
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile  
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala  
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp  
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val  
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala  
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp  
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu  
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro  
 500 505 510

Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys  
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val  
 530 535 540

Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu  
 545 550 555 560

Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro  
 565 570 575

Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg  
 580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg  
 595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu



610	615	620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His		
625	630	635 640
Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp		
	645	650 655
Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu		
	660	665 670
Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu		
	675	680 685
Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys		
	690	695 700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp		
	705	710 715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly		
	725	730 735
Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys		
	740	745 750
Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser		
	755	760 765
Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala		
	770	775 780
Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln		
	785	790 795 800
Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg		
	805	810 815
Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys		
	820	825 830
Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu		
	835	840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala  
850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln  
865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val  
885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val  
900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu  
915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala  
930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser  
945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala  
965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys  
980 985 990

Arg Gln Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys  
995 1000 1005

<210> 115

<211> 3027

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Drosophila melanogaster

<400> 115

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gtcgcccaaa gcaacttcgc taacgggggtc gctgaatgga tcagctctaa ctgcggttca 120

caggcttaca aagtaacctg tagcggttcgt cagagctctg cgcagaatcg caaatacacc 180

atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gcttcctgta 240

gccgcatggc gttcgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300

gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360  
 tcagcaatcg cagcaaacctc cggcatctac cccatggcaa ctgaagaggc catcatccgc 420  
 atccccccat accactacat ccatgtgctg gaccagaaca gtaatgtgtc ccgtgtggag 480  
 gttggaccaa agacctacat ccggcaggac aatgagaggg tactgtttgc cccagttcgc 540  
 atggtgaccg tccccccacg ccactactgc atagtggcca accctgtgtc ccgggacacc 600  
 cagagttctg tgttatttga catcacagga caagtccgac tccggcacgc tgaccaggag 660  
 atccgactag cccaggaccc cttccccctg tatccagggg aggtgctgga aaaggacatc 720  
 accccactgc aggtgggttct gcccacaca gcaactgcac ttaaggcggt gctggacttt 780  
 gaggataaga atggagacaa ggtcatggca ggagacgagt ggctatttga gggacctggc 840  
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 gaagaggtgc tggatctggt ggatgctgtg atccttacag aaaagactgc cctgcacctc 1080  
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 gtctatgact acagagccaa gagagcccgt gtggtctttg ggcccagct agtgacactg 1860  
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 gcccgccgtg cactctgcct actgctggga cctgatttct ttactgatgt catcaccatc 1980  
 gaaactgcag atcatgccag gttgcagctg cagcttgctt acaactggca ctttgaactg 2040

```

aagaaccgga atgaccctgc agaggcagcc aagcttttct cctgcctga cttcgtgggt 2100
gacgcctgca aggccattgc atcccgagtc cggggggctg tagcctctgt cacctttgat 2160
gacttccata aaaactcagc ccggatcatt cgaatggctg tttttggctt tgagatgtct 2220
gaagacacag gtcctgatgg cacactcctg cccaaggctc gagaccaggc agtctttccc 2280
caaaacgggc tggtagtcag cagtgtggat gtgcagtcag tggagcccgt ggaccagagg 2340
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gtggaggcaa agaagttcaa ggagatgaca gaggcactgg gcccggcac catcagggac 2820
ctggctgtgg ccggggccaga gatgcagggtg aaacttctcc agtccctggg cctgaaatcc 2880
actctcatca ccgatggctc gtctcccatc aacctcttca gcacagcctt cgggttgctg 2940
gggctggggg ctgatggtca gccgccagca cagaagcgac agatcaagat ctggtttcag 3000
aacgcacgga tgaagtggaa gaagtga 3027

```

&lt;210&gt; 116

&lt;211&gt; 1273

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Levivirus and Homo sapiens and synthesized

&lt;400&gt; 116

```

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr
1           5           10           15

```

```

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
20           25           30

```

```

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
35           40           45

```

```

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu

```

50                                      55                                      60  
 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
 65                                      70                                      75                                      80  
 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
                                     85                                      90                                      95  
 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
                                     100                                      105                                      110  
 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
                                     115                                      120                                      125  
 Ile Tyr Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr  
                                     130                                      135                                      140  
 His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu  
 145                                      150                                      155                                      160  
 Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe  
                                     165                                      170                                      175  
 Ala Pro Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val  
                                     180                                      185                                      190  
 Ala Asn Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val  
                                     195                                      200                                      205  
 Thr Gly Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala  
                                     210                                      215                                      220  
 Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile  
 225                                      230                                      235                                      240  
 Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala  
                                     245                                      250                                      255  
 Leu Leu Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp  
                                     260                                      265                                      270  
 Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val  
                                     275                                      280                                      285

Glu Val Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala  
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp  
 355 360 365

Phe Arg Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu  
 435 440 445

Gln Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Arg Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro  
 500 505 510

Leu Asp Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys  
 515 520 525

Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val  
530 535 540

Leu Trp Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys  
545 550 555 560

Gly Gln Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser  
565 570 575

Leu Gln Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg  
580 585 590

Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg  
595 600 605

Ala Arg Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu  
610 615 620

Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His  
625 630 635 640

Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp  
645 650 655

Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu  
660 665 670

Ala Tyr Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu  
675 680 685

Thr Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys  
690 695 700

Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp  
705 710 715 720

Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly  
725 730 735

Phe Glu Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg  
740 745 750

Pro Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser

755					760					765									
Val	Asp	Val	Gln	Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala				
770					775					780									
Leu	Gln	Arg	Ser	Val	Gln	Leu	Ala	Ile	Glu	Ile	Thr	Thr	Asn	Ser	Gln				
785					790					795					800				
Glu	Ala	Ala	Ala	Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg				
805					810					815									
Gly	Arg	Leu	Glu	Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys				
820					825					830									
Ala	Arg	Lys	Glu	Leu	Leu	Glu	Leu	Glu	Ala	Leu	Ser	Met	Ala	Val	Glu				
835					840					845									
Ser	Thr	Gly	Thr	Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala				
850					855					860									
Arg	Ile	Glu	Gly	Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln				
865					870					875					880				
Ala	Leu	Ala	Ile	Glu	Thr	Glu	Ala	Glu	Leu	Gln	Arg	Val	Gln	Lys	Val				
885					890					895									
Arg	Glu	Leu	Glu	Leu	Val	Tyr	Ala	Arg	Ala	Gln	Leu	Glu	Leu	Glu	Val				
900					905					910									
Ser	Lys	Ala	Gln	Gln	Leu	Ala	Glu	Val	Glu	Val	Lys	Lys	Phe	Lys	Gln				
915					920					925									
Met	Thr	Glu	Ala	Ile	Gly	Pro	Ser	Thr	Ile	Arg	Asp	Leu	Ala	Val	Ala				
930					935					940									
Gly	Pro	Glu	Met	Gln	Val	Lys	Leu	Leu	Gln	Ser	Leu	Gly	Leu	Lys	Ser				
945					950					955					960				
Thr	Leu	Ile	Thr	Asp	Gly	Ser	Thr	Pro	Ile	Asn	Leu	Phe	Asn	Thr	Ala				
965					970					975									
Phe	Gly	Leu	Leu	Gly	Met	Gly	Pro	Glu	Gly	Gln	Pro	Leu	Gly	Arg	Arg				
980					985					990									



Val Ala Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala  
 995 1000 1005

Gln Ala Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu  
 1010 1015 1020

Arg Asp Ile Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser  
 1025 1030 1035

Leu Gly Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val  
 1040 1045 1050

Asp Ile Phe Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro  
 1055 1060 1065

Gly Gln Pro Pro Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu  
 1070 1075 1080

Ser Gly Ile Pro Val Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp  
 1085 1090 1095

Phe Thr Leu Ile Ile Asp Pro Val Glu Ala Asp Asp Val Ala Thr  
 1100 1105 1110

Tyr Tyr Cys Gln Gln Thr Asn Glu Asp Pro Tyr Thr Phe Gly Gly  
 1115 1120 1125

Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr Ser Gly Gly Gly Ser  
 1130 1135 1140

Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu Val Gln Leu Gln  
 1145 1150 1155

Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys Leu  
 1160 1165 1170

Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His  
 1175 1180 1185

Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg  
 1190 1195 1200

Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln  
 1205 1210 1215

Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr  
 1220 1225 1230

Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr  
 1235 1240 1245

Cys Ala Pro Phe Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr  
 1250 1255 1260

Trp Gly Gln Gly Thr Ser Val Thr Val Ser  
 1265 1270

<210> 117  
 <211> 3822  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Levivirus and Homo sapiens and synthesized

<400> 117  
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 caggcttaca aagtaacctg tagcgttcgt cagagctctg cgcagaatcg caaatacacc 180  
 atcaaagtcg aggtgcctaa agtggcaacc cagactgttg gtggtgtaga gcttcctgta 240  
 gccgcatggc gtctgtactt aaatatggaa ctaaccattc caattttcgc tacgaattcc 300  
 gactgcgagc ttattgttaa ggcaatgcaa ggtctcctaa aagatggaaa cccgattccc 360  
 tcagcaatcg cagcaaactc cggcatctac cccatggcaa ctgaagagtt catcatccgc 420  
 atccccccat accactatat ccatgtgctg gaccagaaca gcaacgtgtc ccgtgtggag 480  
 gtcggggcaa agacctacat ccggcaggac aatgagaggg tactgtttgc ccccatgcgc 540  
 atggtgaccg tccccccacg tctactactgc acagtggcca accctgtgtc tcgggatgcc 600  
 cagggttgg tgctgtttga tgtcacaggg caagttcggc ttcgccacgc tgacctcgag 660  
 atccggctgg cccaggaccc ctccccctg taccagggg aggtgctgga aaaggacatc 720  
 acaccctgc aggtggttct gcccaacact gccctccatc taaaggcgct gcttgatttt 780  
 gaggataaag atggagacaa ggtggtggca ggagatgagt ggcttttcga gggacctggc 840  
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&lt;210&gt; 118

&lt;211&gt; 1241

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Levivirus and Rattus norvegicus and synthesized

&lt;400&gt; 118

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr  
 1 5 10 15

Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
 20 25 30

Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser

35	40	45
Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu		
50	55	60
Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val		
65	70	75
Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe		
85	90	95
Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu		
100	105	110
Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly		
115	120	125
Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr		
130	135	140
His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu		
145	150	155
Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe		
165	170	175
Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val		
180	185	190
Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile		
195	200	205
Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala		
210	215	220
Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile		
225	230	235
Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala		
245	250	255
Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp		
260	265	270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val  
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala  
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp  
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu  
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro  
 500 505 510

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<210> 126

<211> 1003

<212> PRT

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Human immunodeficiency virus type 1

<400> 126

Met Ala Ser Asn Phe Thr Gln Phe Val Leu Val Asp Asn Gly Gly Thr  
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Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu  
 20 25 30



Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser  
 35 40 45

Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu  
 50 55 60

Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val  
 65 70 75 80

Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe  
 85 90 95

Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu  
 100 105 110

Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly  
 115 120 125

Ile Tyr Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr  
 130 135 140

His Tyr Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu  
 145 150 155 160

Val Gly Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe  
 165 170 175

Ala Pro Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val  
 180 185 190

Ala Asn Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile  
 195 200 205

Thr Gly Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala  
 210 215 220

Gln Asp Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile  
 225 230 235 240

Thr Pro Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala  
 245 250 255

Leu Leu Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp  
 260 265 270

Glu Trp Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val  
 275 280 285

Glu Val Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala  
 290 295 300

Leu Arg Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly  
 305 310 315 320

Arg Val Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu  
 325 330 335

Pro Ala Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu  
 340 345 350

Thr Glu Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp  
 355 360 365

Leu Arg Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val  
 370 375 380

Gln Asp Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly  
 385 390 395 400

Val Val Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu  
 405 410 415

Asp Pro Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val  
 420 425 430

Val Lys Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu  
 435 440 445

Arg Gly Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu  
 450 455 460

Leu Lys Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val  
 465 470 475 480

Ser His Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr  
 485 490 495

Val Pro Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro

500	505	510
Leu Asp Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys 515	520	525
Val Arg Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val 530	535	540
Leu Trp Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu 545	550	555 560
Gly His Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro 565	570	575
Leu Gln Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg 580	585	590
Val Pro His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg 595	600	605
Ala Arg Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu 610	615	620
Gln Phe Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His 625	630	635 640
Ala Arg Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp 645	650	655
Val Ile Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu 660	665	670
Ala Tyr Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu 675	680	685
Ala Ala Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys 690	695	700
Ala Ile Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp 705	710	715 720
Asp Phe His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly 725	730	735

Phe Glu Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys  
 740 745 750

Ala Arg Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser  
 755 760 765

Val Asp Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala  
 770 775 780

Leu Gln Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln  
 785 790 795 800

Glu Ala Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg  
 805 810 815

Gly Arg Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys  
 820 825 830

Ala Arg Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu  
 835 840 845

Ser Thr Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala  
 850 855 860

Arg Ile Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln  
 865 870 875 880

Ala Leu Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val  
 885 890 895

Arg Glu Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val  
 900 905 910

Ser Lys Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu  
 915 920 925

Met Thr Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala  
 930 935 940

Gly Pro Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser  
 945 950 955 960

Thr Leu Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala  
 965 970 975

Phe Gly Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys  
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Tyr Gly Arg Lys Lys Arg Arg Gln Arg Arg Arg  
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<210> 127

<211> 3012

<212> DNA

<213> Artificial Sequence

<220>

<223> Levivirus and Rattus norvegicus and Human immunodeficiency virus  
           type 1

<400> 127

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actctcatca	ccgatggctc	gtctcccatc	aacctcttca	gcacagcctt	cgggttgctg	2940

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<210> 128  
<211> 926  
<212> PRT  
<213> Artificial Sequence

<220>  
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<400> 128

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20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly  
35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro  
50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn  
65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly  
85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp  
100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp  
145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val  
165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala  
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg  
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val  
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro  
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His  
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415



Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
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Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln  
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Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln  
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Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala  
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu  
 610 615 620

Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg  
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp

645	650	655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln		
660	665	670
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
675	680	685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
690	695	700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
705	710	715
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr		
725	730	735
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
740	745	750
Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu		
755	760	765
Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu		
770	775	780
Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys		
785	790	795
Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr		
805	810	815
Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro		
820	825	830
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu		
835	840	845
Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly		
850	855	860
Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala		
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		880

Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys  
915 920 925

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<211>	2781
<212>	DNA
<213>	Artificial Sequence

<220>  
<223> synthesized and Homo sapiens and Drosophila melanogaster

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cctgtgtctc	gggatgccc	gggcttggtg	ctgtttgatg	tcacagggca	agttcggctt	300
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&lt;210&gt; 130

&lt;211&gt; 894

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and Rattus norvegicus and Drosophila melanogaster

&lt;400&gt; 130

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys  
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Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr  
 20 25 30

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly  
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro  
 50 55 60

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn  
 65 70 75 80

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly  
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp  
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val  
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val

195	200	205
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala		
210	215	220
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu		
225	230	235 240
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg		
245	250	255
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp		
260	265	270
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val		
275	280	285
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro		
290	295	300
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys		
305	310	315 320
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly		
325	330	335
Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys		
340	345	350
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His		
355	360	365
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro		
370	375	380
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp		
385	390	395 400
Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg		
405	410	415
Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp		
420	425	430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His  
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln  
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala  
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu  
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg  
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp  
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln  
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala  
675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg  
690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg  
705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr  
725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile  
740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu  
755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu  
770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys  
785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr  
805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro  
820 825 830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu  
835 840 845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly  
850 855 860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Arg Gln  
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Ile Lys Ile Trp Phe Gln Asn Ala Arg Met Lys Trp Lys Lys  
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<210> 131



<211> 2685  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> synthesized and *Rattus norvegicus* and *Drosophila melanogaster*

<400> 131

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<210> 132

<211> 1159

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens

<400> 132

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          20          25          30

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly  
 35 40 45

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro  
 50 55 60

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn  
 65 70 75 80

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly  
 85 90 95

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp  
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val  
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala  
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg  
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val  
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro  
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His  
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
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Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln  
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Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln  
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Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
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His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe

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Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg 515	520	525
Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile 530	535	540
Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr 545	550	555 560
Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala 565	570	575
Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile 580	585	590
Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe 595	600	605
His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu 610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg 625	630	635 640
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp 645	650	655
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln 660	665	670
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala 675	680	685
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg 690	695	700
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg 705	710	715 720
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr 725	730	735

Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile  
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Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu  
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Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu  
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Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys  
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Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr  
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Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro  
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Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu  
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Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly  
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Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala  
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Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala  
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Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Asp Ile  
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Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg  
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Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val  
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Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu  
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Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe  
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Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser  
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Thr Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser  
           1025                                  1030                                  1035

Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro  
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Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile  
           1055                                  1060                                  1065

Lys Asp Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly  
           1070                                  1075                                  1080

Leu Glu Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys  
           1085                                  1090                                  1095

Tyr Val Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr  
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Ser Ser Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu  
           1115                                  1120                                  1125

Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe Gly Tyr Tyr Val Ser  
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&lt;400&gt; 133

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Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly  
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Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro  
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Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn  
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Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly  
85 90 95

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp  
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Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp  
145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val  
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Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala  
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Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
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Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg  
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Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val  
 275 280 285

Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro  
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Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His  
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Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
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Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
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Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
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Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His  
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Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln  
450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg  
485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe  
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Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
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Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala  
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Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
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Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
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His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu  
610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg  
625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp

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Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala		
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Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg		
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Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg		
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Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr		
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Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile		
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Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu		
755	760	765
Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu		
770	775	780
Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys		
785	790	795
Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr		
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Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro		
820	825	830
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu		
835	840	845
Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly		
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Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Asp Ile		
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Val Leu Thr Gln Ser Pro Ala Ser Leu Ala Val Ser Leu Gly Gln Arg  
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Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe Gly Val  
                   900                                  905                  910

Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro Lys Leu  
                   915                                  920                  925

Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val Arg Phe  
                   930                                  935                  940

Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp Pro Val  
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Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn Glu Asp  
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Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly Ser Thr  
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Ser Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Gly Ser Ser Glu  
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Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala  
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Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp  
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Thr Tyr Met His Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu  
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Trp Ile Gly Arg Ile Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val  
                   1055                                  1060                  1065

Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser  
                   1070                                  1075                  1080

Asn Thr Ala Tyr Leu Gln Leu Thr Ser Leu Thr Ser Glu Asp Thr  
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tattattgtg ctccgtttgg ttactacgtg tctgactatg ctatggccta ctgggggtcaa 3360
ggaacctcag tcaccgtctc gtga 3384

```

&lt;210&gt; 136

&lt;211&gt; 966

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthesized and two Homo sapiens sequences

&lt;400&gt; 136

```

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

```

```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35          40          45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50          55          60

```

```

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65          70          75          80

```

```

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
          85          90          95

```

```

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp
          100          105          110

```

```

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro
          115          120          125

```

```

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu
          130          135          140

```

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val  
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala  
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg  
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val  
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro  
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His  
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln  
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln  
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala  
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Thr Ala Val Phe Gly Phe Glu

610	615	620
Thr Ser Glu Ala Lys Gly Pro Asp Gly Met Ala Leu Pro Arg Pro Arg 625 630 635 640		
Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp 645 650 655		
Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln 660 665 670		
Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala 675 680 685		
Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg 690 695 700		
Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg 705 710 715 720		
Lys Glu Leu Leu Glu Leu Glu Ala Leu Ser Met Ala Val Glu Ser Thr 725 730 735		
Gly Thr Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile 740 745 750		
Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu 755 760 765		
Ala Ile Glu Thr Glu Ala Glu Leu Gln Arg Val Gln Lys Val Arg Glu 770 775 780		
Leu Glu Leu Val Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys 785 790 795 800		
Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr 805 810 815		
Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro 820 825 830		
Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu 835 840 845		

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly  
850 855 860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala  
865 870 875 880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala  
885 890 895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Met Gly  
900 905 910

Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His  
915 920 925

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn  
930 935 940

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys  
945 950 955 960

Trp Trp Glu Leu Arg Ala  
965

<210> 137  
<211> 2901  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> synthesized and two Homo sapiens sequences

<400> 137  
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aacgtgtccc gtgtggaggt cgggccaaag acctacatcc ggcaggacaa tgagagggtg 180  
ctgtttgccc ccatgcgcat ggtgaccgtc cccccacgtc actactgcac agtggccaac 240  
cctgtgtctc gggatgccca gggcttggtg ctgtttgatg tcacagggca agttcggctt 300  
cgccacgctg acctcgagat cgggctggcc caggaccctt tccccctgta ccagggggag 360  
gtgctggaaa aggacatcac acccctgcag gtggttctgc ccaacactgc cctccatcta 420  
aaggcgctgc ttgattttga ggataaagat ggagacaagg tggaggcagg agatgagtgg 480  
cttttcgagg gacctggcac gtacatcccc cggaaggaag tggaggtcgt ggagatcatt 540

caggccacca tcatcaggca gaaccaggct ctgcggtcca gggcccgcaa ggagtgtctgg 600  
gaccgggacg gcaaggagag ggtgacaggg gaagaatggc tggtcaccac agtaggggag 660  
tacctcccag cgggtgttga ggaggttctg gatttggtgg acgccgtcat ccttacggaa 720  
aagacagccc tgcacctccg ggctcggcgg aacttcggg acttcagggg agtgtcccgc 780  
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attctcgacc ctgtcggacc ggatggcaag aatcagctgg ggcagaagcg cgtggtcaag 960  
ggagagaagt cttttttcct ccagccagga gagcagctgg aacaaggcat ccaggatgtg 1020  
tatgtgtgt cggagcagca ggggtgtctg ctgagggccc tgcagcccct ggaggagggg 1080  
gaggatgagg agaaggtctc acaccaggct ggggaccact ggctcatccg cggaccctg 1140  
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gagaacgagg gcatctatgt gcaggatgtc aagaccggaa aggtgcgcgc tgtgattgga 1260  
agcacctaca tgctgacca ggacgaagtc ctgtgggaga aagagctgcc tcccgggggtg 1320  
gaggagctgc tgaacaaggg gcaggaccct ctggcagaca ggggtgagaa ggacacagct 1380  
aagagcctcc agcccttggc gccccggaac aagaccctg tggtcagcta ccgctgccc 1440  
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cctgagctgg tgctgctggg tcctgaggag cagttcacag tgttgtccct ctgagctggg 1560  
cgcccaagc gtcccatgc ccgctgctg ctctgcctgc tgctggggcc tgacttcttc 1620  
acagacgtca tcaccatcga aacggcggat catgccaggc tgcaactgca gctggcctac 1680  
aactggcact ttgaggtgaa tgaccggaag gaccccaag agacggccaa gctcttttca 1740  
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gaccaggctg tcttccccca aaacgggctg gtggtcagca gtgtggacgt gcagtcaagt 1980  
gagcctgtgg atcagaggac ccgggacgcc ctgcaacgca gcgtccagct ggccatcgag 2040  
atcaccacca actcccagga agcggcggcc aagcatgagg ctgagagact ggagcaggaa 2100  
gcccgcggcc ggcttgagcg gcagaagatc ctggaccagt cagaagccga gaaagctcgc 2160  
aaggaacttt tggagctgga ggctctgagc atggcctggt agagcaccgg gactgccaa 2220  
gcggaggccg agtcccgtgc ggaggcagcc cggattgagg gagaagggtc cgtgctgcag 2280

```

gccaaagctaa aagcacaggc cttggccatt gaaacggagg ctgagctcca gaggggtccag 2340
aagggtccgag agctggaact ggtctatgcc cgggcccagc tggagctgga ggtgagcaag 2400
gctcagcagc tggctgaggt ggaggtgaag aagttcaagc agatgacaga ggccataggc 2460
cccagcacca tcagggacct tgctgtggct gggcctgaga tgcaggtaaa actgctccag 2520
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tctcagcagc gttattgcct gcatgatggt gtttgtatgt atatcgaagc tctggacaaa 2820
tatgcttgca actgtgttgt tggttacatc ggtgagcgtt gccagtatcg cgacctgaaa 2880
tggtgggaac tgcgtgcatg a 2901

```

<210> 138  
 <211> 934  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Rattus norvegicus and Homo sapiens  
 <400> 138

```

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1           5           10           15

```

```

Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
           20           25           30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
           35           40           45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
           50           55           60

```

```

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
65           70           75           80

```

```

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
           85           90           95

```

```

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp

```

100	105	110
Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro		
115	120	125
Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu		
130	135	140
Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp		
145	150	155
Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val		
165	170	175
Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg		
180	185	190
Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val		
195	200	205
Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala		
210	215	220
Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu		
225	230	235
Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg		
245	250	255
Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp		
260	265	270
Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val		
275	280	285
Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro		
290	295	300
Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys		
305	310	315
Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly		
325	330	335



Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His  
 355 360 365

Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
 385 390 395 400

Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
 420 425 430

Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His  
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln  
 450 455 460

Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
 545 550 555 560

Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala  
 565 570 575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu  
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg  
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp  
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln  
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala  
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg  
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg  
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr  
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile  
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu  
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu  
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys  
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr

805					810					815					
Glu	Ala	Leu	Gly	Pro	Gly	Thr	Ile	Arg	Asp	Leu	Ala	Val	Ala	Gly	Pro
			820					825					830		
Glu	Met	Gln	Val	Lys	Leu	Leu	Gln	Ser	Leu	Gly	Leu	Lys	Ser	Thr	Leu
			835				840					845			
Ile	Thr	Asp	Gly	Ser	Ser	Pro	Ile	Asn	Leu	Phe	Ser	Thr	Ala	Phe	Gly
			850				855					860			
Leu	Leu	Gly	Leu	Gly	Ser	Asp	Gly	Gln	Pro	Pro	Ala	Gln	Lys	Met	Gly
			865				870					875			880
Asn	Ser	Asp	Ser	Glu	Cys	Pro	Leu	Ser	His	Asp	Gly	Tyr	Cys	Leu	His
				885					890					895	
Asp	Gly	Val	Cys	Met	Tyr	Ile	Glu	Ala	Leu	Asp	Lys	Tyr	Ala	Cys	Asn
			900					905					910		
Cys	Val	Val	Gly	Tyr	Ile	Gly	Glu	Arg	Cys	Gln	Tyr	Arg	Asp	Leu	Lys
			915				920					925			
Trp	Trp	Glu	Leu	Arg	Ala										
			930												

<210> 139  
 <211> 2805  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Rattus norvegicus and Homo sapiens

<400> 139  
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 aatgtgtccc gtgtggaggt tggaccaaag acctacatcc ggcaggacaa tgagagggta 180  
 ctgtttgccc cagttcgcgc ggtgaccgtc cccccacgcc actactgcat agtggccaac 240  
 cctgtgtccc gggacaccca gagttctgtg ttatttgaca tcacaggaca agtccgactc 300  
 cggcacgctg accaggagat ccgactagcc caggaccctt tccccctgta tccagggggag 360  
 gtgctggaaa aggacatcac ccactgcag gtggttctgc ccaacacagc actgcatctt 420

aaggcggttgc tggactttga ggataagaat ggagacaagg tcatggcagg agacgagtgg	480
ctattttgagg gacctggcac ctacatccca cagaaggaag tggaagtcgt ggagatcatt	540
caggccacag tcatcaaaca gaaccaagca ctgcggtctaa gggcccgaag ggagtgtttt	600
gaccgggagg gcaaggggag cgtgacaggt gaggagtggc tggtcggatc cgtggggggt	660
tacctcccag ctgtctttga agagggtgctg gatctgggtg atgctgtgat ccttacagaa	720
aagactgccc tgcacctccg ggctctgcag aacttcaggg accttcgggg agtgctccac	780
cgcaccgggg aggaatgggt agtgacagtg caggacacag aagcccatgt tccagatgtc	840
tatgaggagg tgcttggggg agtacctatc accacctgg gacctcgaca ctactgtgtc	900
attcttgacc caatgggacc agacggcaag aaccagctgg gacaaaagcg tgttgtcaag	960
ggagagaagt cctttttcct ccagccagga gagaggctgg agcgaggcat ccaggatgtg	1020
tatgtgtgtg cagagcagca ggggctgcta ctgaaggcac tgcagcccct ggaggaggga	1080
gagagcgagg agaaggtctc ccatcaggcc ggagactgct ggctcatccg tgggcccctg	1140
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agcacctaca tgctgactca ggatgaagtc ctgtgggaaa aggagctgcc ttctgggggtg	1320
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aagccccctc agccctcagc tccaaggaac aagaccgag tggtcagcta ccgtgtcccg	1440
cacaatgcag cgggtgcaggt ctatgactac agagccaaga gagcccgtgt ggtctttggg	1500
cccgagctag tgacactgga tcctgaggag cagttcacag tattgtccct ttctgccggg	1560
cgacccaagc gtcctcatgc ccgccgtgca ctctgcctac tgctgggacc tgatttcttt	1620
actgatgtca tcaccatcga aactgcagat catgccaggt tgcagctgca gcttgccctac	1680
aactggcact ttgaactgaa gaaccggaat gacctgcag aggcagccaa gcttttctcc	1740
gtgcctgact tcgtgggtga cgctgcaag gccattgcat cccgagtcgg gggggctgta	1800
gcctctgtca cttttgatga cttccataaa aactcagccc ggatcattcg aatggctgtt	1860
tttggtttg agatgtctga agacacaggt cctgatggca cactcctgcc caaggctcga	1920
gaccaggcag tctttcccca aaacgggctg gtagtcagca gtgtggatgt gcagtcagt	1980
gagcccgtgg accagaggac ccgggatgcc cttcagcgca gcgttcagct ggccatcgaa	2040
attaccacca actcccagga ggcagcagcc aagcacgagg ctgagagact ggaacaggaa	2100
gcccgtggtc ggcttgagag gcagaagatc ttggaccagt cagaagctga aaaagcccgc	2160

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gccaagctca aggcacaggc gctagccatt gagacggagg ctgagttgga gcgagtaaag 2340
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gcgcagcagc ttgccaatgt ggaggcaaag aagttcaagg agatgacaga ggcactgggc 2460
cccggcacca tcagggacct ggctgtggcc gggccagaga tgcaggtgaa acttctccag 2520
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<210> 140

<211> 921

<212> PRT

<213> Artificial Sequence

<220>

<223> synthesized and Homo sapiens and Human immunodeficiency virus  
type 1

<400> 140

```

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1           5           10           15

```

```

Pro Met Ala Thr Glu Glu Phe Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20           25           30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35           40           45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50           55           60

```

```

Met Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Thr Val Ala Asn
65           70           75           80

```

```

Pro Val Ser Arg Asp Ala Gln Gly Leu Val Leu Phe Asp Val Thr Gly
          85           90           95

```

Gln Val Arg Leu Arg His Ala Asp Leu Glu Ile Arg Leu Ala Gln Asp  
 100 105 110

Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
 130 135 140

Asp Phe Glu Asp Lys Asp Gly Asp Lys Val Val Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Arg Lys Glu Val Glu Val  
 165 170 175

Val Glu Ile Ile Gln Ala Thr Ile Ile Arg Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Trp Asp Arg Asp Gly Lys Glu Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Thr Thr Val Gly Ala Tyr Leu Pro Ala  
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Arg Arg Asn Phe Arg Asp Phe Arg  
 245 250 255

Gly Val Ser Arg Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val His Glu Glu Val Leu Gly Val Val  
 275 280 285

Pro Ile Thr Thr Leu Gly Pro His Asn Tyr Cys Val Ile Leu Asp Pro  
 290 295 300

Val Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Gln Leu Glu Gln Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Arg  
 340 345 350

Ala Leu Gln Pro Leu Glu Glu Gly Glu Asp Glu Glu Lys Val Ser His  
 355 360 365

Gln Ala Gly Asp His Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro  
 370 375 380

Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp  
 385 390 395 400

Glu Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg  
 405 410 415

Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp  
 420 425 430

Glu Lys Glu Leu Pro Pro Gly Val Glu Glu Leu Leu Asn Lys Gly Gln  
 435 440 445

Asp Pro Leu Ala Asp Arg Gly Glu Lys Asp Thr Ala Lys Ser Leu Gln  
 450 455 460

Pro Leu Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro  
 465 470 475 480

His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Glu Lys Arg Ala Arg  
 485 490 495

Val Val Phe Gly Pro Glu Leu Val Ser Leu Gly Pro Glu Glu Gln Phe  
 500 505 510

Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg  
 515 520 525

Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile  
 530 535 540

Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr  
 545 550 555 560

Asn Trp His Phe Glu Val Asn Asp Arg Lys Asp Pro Gln Glu Thr Ala

565					570					575					
Lys	Leu	Phe	Ser	Val	Pro	Asp	Phe	Val	Gly	Asp	Ala	Cys	Lys	Ala	Ile
			580					585					590		
Ala	Ser	Arg	Val	Arg	Gly	Ala	Val	Ala	Ser	Val	Thr	Phe	Asp	Asp	Phe
			595				600					605			
His	Lys	Asn	Ser	Ala	Arg	Ile	Ile	Arg	Thr	Ala	Val	Phe	Gly	Phe	Glu
	610					615					620				
Thr	Ser	Glu	Ala	Lys	Gly	Pro	Asp	Gly	Met	Ala	Leu	Pro	Arg	Pro	Arg
625					630					635					640
Asp	Gln	Ala	Val	Phe	Pro	Gln	Asn	Gly	Leu	Val	Val	Ser	Ser	Val	Asp
				645					650					655	
Val	Gln	Ser	Val	Glu	Pro	Val	Asp	Gln	Arg	Thr	Arg	Asp	Ala	Leu	Gln
			660					665					670		
Arg	Ser	Val	Gln	Leu	Ala	Ile	Glu	Ile	Thr	Thr	Asn	Ser	Gln	Glu	Ala
			675				680					685			
Ala	Ala	Lys	His	Glu	Ala	Gln	Arg	Leu	Glu	Gln	Glu	Ala	Arg	Gly	Arg
	690					695					700				
Leu	Glu	Arg	Gln	Lys	Ile	Leu	Asp	Gln	Ser	Glu	Ala	Glu	Lys	Ala	Arg
705					710					715					720
Lys	Glu	Leu	Leu	Glu	Leu	Glu	Ala	Leu	Ser	Met	Ala	Val	Glu	Ser	Thr
				725					730					735	
Gly	Thr	Ala	Lys	Ala	Glu	Ala	Glu	Ser	Arg	Ala	Glu	Ala	Ala	Arg	Ile
			740					745					750		
Glu	Gly	Glu	Gly	Ser	Val	Leu	Gln	Ala	Lys	Leu	Lys	Ala	Gln	Ala	Leu
		755					760					765			
Ala	Ile	Glu	Thr	Glu	Ala	Glu	Leu	Gln	Arg	Val	Gln	Lys	Val	Arg	Glu
	770					775					780				
Leu	Glu	Leu	Val	Tyr	Ala	Arg	Ala	Gln	Leu	Glu	Leu	Glu	Val	Ser	Lys
785					790					795					800



Ala Gln Gln Leu Ala Glu Val Glu Val Lys Lys Phe Lys Gln Met Thr  
                     805                    810                    815

Glu Ala Ile Gly Pro Ser Thr Ile Arg Asp Leu Ala Val Ala Gly Pro  
                     820                    825                    830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu  
                     835                    840                    845

Ile Thr Asp Gly Ser Thr Pro Ile Asn Leu Phe Asn Thr Ala Phe Gly  
                     850                    855                    860

Leu Leu Gly Met Gly Pro Glu Gly Gln Pro Leu Gly Arg Arg Val Ala  
                     865                    870                    875                    880

Ser Gly Pro Ser Pro Gly Glu Gly Ile Ser Pro Gln Ser Ala Gln Ala  
                     885                    890                    895

Pro Gln Ala Pro Gly Asp Asn His Val Val Pro Val Leu Arg Tyr Gly  
                     900                    905                    910

Arg Lys Lys Arg Arg Gln Arg Arg Arg  
                     915                    920

<210> 141  
 <211> 2766  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> synthesized and Homo sapiens and Human immunodeficiency virus  
           type 1

<400> 141  
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 aacgtgtccc gtgtggaggt cgggccaaag acctacatcc ggcaggacaa tgagagggta 180  
 ctgtttgccc ccatgcgcat ggtgaccgtc cccccacgtc actactgcac agtggccaac 240  
 cctgtgtctc gggatgccca gggcttggtg ctgtttgatg tcacagggca agttcggctt 300  
 cgccacgctg acctcgagat ccggctggcc caggaccctt tccccctgta ccagggggag 360  
 gtgctggaaa aggacatcac acccctgcag gtggtttctgc ccaacactgc cctccatcta 420  
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cttttcgagg gacctggcac gtacatcccc cggaaggaag tggaggtcgt ggagatcatt	540
caggccacca tcatcaggca gaaccaggct ctgcggctca gggcccgcga ggagtgtctg	600
gaccgggacg gcaaggagag ggtgacaggg gaagaatggc tggtcaccac agtaggggag	660
tacctcccag cgggtgtttga ggaggttctg gatttggtgg acgccgtcat ccttacggaa	720
aagacagccc tgcacctccg ggctcggcgg aacttcgggg acttcagggg agtgtcccgc	780
cgcactgggg aggagtggct ggtaacagtg caggacacag aggccacgt gccagatgtc	840
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cctgagctgg tgtcgtggg tcctgaggag cagttcacag tgttgtccct ctgagctggg	1560
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gcccgcggcc ggcttgagcg gcagaagatc ctggaccagt cagaagccga gaaagctcgc	2160
aaggaacttt tggagctgga ggctctgagc atggccgtgg agagcaccgg gactgccaag	2220

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gcggaggccg agtcccgtgc ggaggcagcc cggattgagg gagaagggtc cgtgctgcag 2280
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cggtga 2766

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&lt;210&gt; 142

&lt;211&gt; 889

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> synthesized and Rattus norvegicus and Human immunodeficiency  
virus type 1

&lt;400&gt; 142

```

Met Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
1          5          10          15

```

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Pro Met Ala Thr Glu Glu Ala Ile Ile Arg Ile Pro Pro Tyr His Tyr
          20          25          30

```

```

Ile His Val Leu Asp Gln Asn Ser Asn Val Ser Arg Val Glu Val Gly
          35          40          45

```

```

Pro Lys Thr Tyr Ile Arg Gln Asp Asn Glu Arg Val Leu Phe Ala Pro
          50          55          60

```

```

Val Arg Met Val Thr Val Pro Pro Arg His Tyr Cys Ile Val Ala Asn
65          70          75          80

```

```

Pro Val Ser Arg Asp Thr Gln Ser Ser Val Leu Phe Asp Ile Thr Gly
          85          90          95

```

```

Gln Val Arg Leu Arg His Ala Asp Gln Glu Ile Arg Leu Ala Gln Asp
          100          105          110

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Pro Phe Pro Leu Tyr Pro Gly Glu Val Leu Glu Lys Asp Ile Thr Pro  
 115 120 125

Leu Gln Val Val Leu Pro Asn Thr Ala Leu His Leu Lys Ala Leu Leu  
 130 135 140

Asp Phe Glu Asp Lys Asn Gly Asp Lys Val Met Ala Gly Asp Glu Trp  
 145 150 155 160

Leu Phe Glu Gly Pro Gly Thr Tyr Ile Pro Gln Lys Glu Val Glu Val  
 165 170 175

Val Glu Ile Ile Gln Ala Thr Val Ile Lys Gln Asn Gln Ala Leu Arg  
 180 185 190

Leu Arg Ala Arg Lys Glu Cys Phe Asp Arg Glu Gly Lys Gly Arg Val  
 195 200 205

Thr Gly Glu Glu Trp Leu Val Arg Ser Val Gly Ala Tyr Leu Pro Ala  
 210 215 220

Val Phe Glu Glu Val Leu Asp Leu Val Asp Ala Val Ile Leu Thr Glu  
 225 230 235 240

Lys Thr Ala Leu His Leu Arg Ala Leu Gln Asn Phe Arg Asp Leu Arg  
 245 250 255

Gly Val Leu His Arg Thr Gly Glu Glu Trp Leu Val Thr Val Gln Asp  
 260 265 270

Thr Glu Ala His Val Pro Asp Val Tyr Glu Glu Val Leu Gly Val Val  
 275 280 285

Pro Ile Thr Thr Leu Gly Pro Arg His Tyr Cys Val Ile Leu Asp Pro  
 290 295 300

Met Gly Pro Asp Gly Lys Asn Gln Leu Gly Gln Lys Arg Val Val Lys  
 305 310 315 320

Gly Glu Lys Ser Phe Phe Leu Gln Pro Gly Glu Arg Leu Glu Arg Gly  
 325 330 335

Ile Gln Asp Val Tyr Val Leu Ser Glu Gln Gln Gly Leu Leu Leu Lys

340	345	350
Ala Leu Gln Pro Leu Glu Glu Gly Glu Ser Glu Glu Lys Val Ser His		
355	360	365
Gln Ala Gly Asp Cys Trp Leu Ile Arg Gly Pro Leu Glu Tyr Val Pro		
370	375	380
Ser Ala Lys Val Glu Val Val Glu Glu Arg Gln Ala Ile Pro Leu Asp		
385	390	395
Gln Asn Glu Gly Ile Tyr Val Gln Asp Val Lys Thr Gly Lys Val Arg		
405	410	415
Ala Val Ile Gly Ser Thr Tyr Met Leu Thr Gln Asp Glu Val Leu Trp		
420	425	430
Glu Lys Glu Leu Pro Ser Gly Val Glu Glu Leu Leu Asn Leu Gly His		
435	440	445
Asp Pro Leu Ala Asp Arg Gly Gln Lys Gly Thr Ala Lys Pro Leu Gln		
450	455	460
Pro Ser Ala Pro Arg Asn Lys Thr Arg Val Val Ser Tyr Arg Val Pro		
465	470	475
His Asn Ala Ala Val Gln Val Tyr Asp Tyr Arg Ala Lys Arg Ala Arg		
485	490	495
Val Val Phe Gly Pro Glu Leu Val Thr Leu Asp Pro Glu Glu Gln Phe		
500	505	510
Thr Val Leu Ser Leu Ser Ala Gly Arg Pro Lys Arg Pro His Ala Arg		
515	520	525
Arg Ala Leu Cys Leu Leu Leu Gly Pro Asp Phe Phe Thr Asp Val Ile		
530	535	540
Thr Ile Glu Thr Ala Asp His Ala Arg Leu Gln Leu Gln Leu Ala Tyr		
545	550	555
Asn Trp His Phe Glu Leu Lys Asn Arg Asn Asp Pro Ala Glu Ala Ala		
565	570	575

Lys Leu Phe Ser Val Pro Asp Phe Val Gly Asp Ala Cys Lys Ala Ile  
 580 585 590

Ala Ser Arg Val Arg Gly Ala Val Ala Ser Val Thr Phe Asp Asp Phe  
 595 600 605

His Lys Asn Ser Ala Arg Ile Ile Arg Met Ala Val Phe Gly Phe Glu  
 610 615 620

Met Ser Glu Asp Thr Gly Pro Asp Gly Thr Leu Leu Pro Lys Ala Arg  
 625 630 635 640

Asp Gln Ala Val Phe Pro Gln Asn Gly Leu Val Val Ser Ser Val Asp  
 645 650 655

Val Gln Ser Val Glu Pro Val Asp Gln Arg Thr Arg Asp Ala Leu Gln  
 660 665 670

Arg Ser Val Gln Leu Ala Ile Glu Ile Thr Thr Asn Ser Gln Glu Ala  
 675 680 685

Ala Ala Lys His Glu Ala Gln Arg Leu Glu Gln Glu Ala Arg Gly Arg  
 690 695 700

Leu Glu Arg Gln Lys Ile Leu Asp Gln Ser Glu Ala Glu Lys Ala Arg  
 705 710 715 720

Lys Glu Leu Leu Glu Leu Glu Ala Met Ser Met Ala Val Glu Ser Thr  
 725 730 735

Gly Asn Ala Lys Ala Glu Ala Glu Ser Arg Ala Glu Ala Ala Arg Ile  
 740 745 750

Glu Gly Glu Gly Ser Val Leu Gln Ala Lys Leu Lys Ala Gln Ala Leu  
 755 760 765

Ala Ile Glu Thr Glu Ala Glu Leu Glu Arg Val Lys Lys Val Arg Glu  
 770 775 780

Met Glu Leu Ile Tyr Ala Arg Ala Gln Leu Glu Leu Glu Val Ser Lys  
 785 790 795 800

Ala Gln Gln Leu Ala Asn Val Glu Ala Lys Lys Phe Lys Glu Met Thr  
 805 810 815

Glu Ala Leu Gly Pro Gly Thr Ile Arg Asp Leu Ala Val Ala Gly Pro  
                   820                                  825                                  830

Glu Met Gln Val Lys Leu Leu Gln Ser Leu Gly Leu Lys Ser Thr Leu  
                   835                                  840                                  845

Ile Thr Asp Gly Ser Ser Pro Ile Asn Leu Phe Ser Thr Ala Phe Gly  
                   850                                  855                                  860

Leu Leu Gly Leu Gly Ser Asp Gly Gln Pro Pro Ala Gln Lys Tyr Gly  
                   865                                  870                                  875                                  880

Arg Lys Lys Arg Arg Gln Arg Arg Arg  
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<210> 143

<211> 2670

<212> DNA

<213> Artificial Sequence

<220>

<223> synthesized and Rattus norvegicus and Human immunodeficiency virus type 1

<400> 143

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